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	RESULT 2 T30568 acetyl-CoA carboxylase (EC 6.4.1.2) - Emericella nidulans C;Species: Emericella nidulans, Aspergillus nidulans C;Species: Emericella nidulans, Aspergillus nidulans C;Species: Emericella nidulans, Aspergillus nidulans C;Accession: T30568 R;Morrice, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B. Curr. Genet. 34, 379-385, 1998 A;Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Aspergil A;Reference number: Z20869; MUID:99087906; PMID:9871120 A;Accession: T30568 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Rose-references: UNDA A;Rose-references: UNDA A;Cross-references: UNIPROT:060033; UNIPARC:UPI000006C49E; EMBL:Y15996; NID:g3021302; PJ C;Genetics: A;Cross-references: UNIPROT:OGA carboxylase: biofin carboxylase homology: linoyl/biofin-C:Superfamily: human acetyl-CoA carboxylase: biofin carboxylase homology: linoyl/biofin-C:Superfamily: human acetyl-CoA	2288; s 0; Gaps VKEIRSIRKWAYET VKEIRSVRKWAYET	65 FGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHA	Db 259 KEEDFINLYNAAANEIPGSPIFIMKLAGNARHLEVQLLADQYGNNISLFGRDCSVQRRHQ 318 Qy 305 KIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQV 364

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N;Alternate names: acetyl-coenzyme A carboxylase
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: T42531

R;Salto, A.; Kazuta, Y.; Toh, H.; Kondo, H.; Tanabe, T.
Submitted to the EMBL Data Library, October 1997
A;Description: Biotin-dependent enzymes in Schizosaccharomyces pombe: clon A;Reference number: Z22171
A;Accession: T42531
A;Accession: T42531
A;Accession: T42531
A;Residues: 1-2279 <SAI>>
A;Residues: 1-2279 <SAI>>
A;Residues: 1-2279 <SAI>>
A;Residues: 1-2279 <SAI>>
A;Residues: 2atalyzes the carboxylation of acetyl-CoA to malonyl-CoA un A;Description: catalyzes the carboxylation of acetyl-CoA to malonyl-CoA un A;Description: catalyzes the carboxylase; biotin carboxylase homology; C;Keywords: biotin metabolism; fatty acid biosynthesis
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; C;Keywords: biotin metabolism; fatty acid biosynthesis; ligase
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Matches 392; Conservative (
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                                                                                                                       Sector acroboxylase (EC 6.4.1.2) - yeast (Saccharomyces cerevisiae)

NiAlternate names: protein N3175; protein YNR016c
C; Species Saccharomyces cerevisiae
C; Date: 27-Apr-1996 #sequence revision 03-May-1996 #text_change 03-Jul-2004
C; Apr-1996 #sequence_revision 03-May-1996 #text_change 03-Jul-2004
C; Apr-1996 #sequence_revision 03-May-1996 #text_change 03-Jul-2004
C; Accession: S63347; S31249
B; Pobl, T.M.
Submitted to the Protein Sequence Database, April 1996
A; Researce number: S63346
A; Accession: S63346
A; Researce number: S63346
A; Researce number: S63346
A; Researce number: S63346
A; Researce number: S1249; Mulp: 92262474; PMID: 135093
A; Accession: S1249
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A; Mulp: 92262474; PMID: 135093
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Pred. No. 6.6e-138
5; Mismatches 88
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acetyl-CoA carboxylase (EC 6.4.1.2) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jan-2002
C;Accession: S41121
R;Ha, J.; Daniel, S.; Kong, I.S.; Park, C.K.; Tae, H.J.; Kim, K.H.
Eur. J. Biochem. 219, 297-306, 1994
A;Title: Cloning of human acetyl-CoA carboxylase cDNA.
A;Title: Cloning of human acetyl-CoA carboxylase cDNA.
A;Accession: S41121
A;Accession: S41121
A;Accession: S41121
A;Residues: 1-2339 <HAJ>
A;Cross-references: UNIPARC:UPI000011EDF5; EMBL:X68968; NID:g452315; PIDN:CAA48770.1; I
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology <BCH>
C;Superfamil: biotin carboxylase homology <BCH>
F;120-620/Domain: biotin carboxylase homology <LPB>
F;747-819/Domain: lipoyl/biotin-binding homology <LPB>
F;746/Binding site: biotin (Lys) (covalent) #status predicted
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Pred. No. 4.4e-118;
3; Mismatches 105;
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Best Local Similarity. 63.6%; Pi
Matches 344; Conservative 78;
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C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_cl C; Accession: A29924; A29337; A27903
R; Takai, T.; Yokoyama, C.; Wada, K.; Tanabe, T.
J; Biol. Chem. 263, 2651-2657, 1988
A; Title: Primary structure of chicken liver acetyl-CoA cark A; Reference number: A29924; MUID:88139305; PMID:2893793
A; Rccession: A29924
A; Molecule type: mRNA
A; Residues: 1-2324
A; Molecule type: mRNA
A; Reference number: A29924; MUID:87106011; PMID:2879745
A; Takai, T.; Wada, K.; Tanabe, T.
FEBS Lett. 212, 98-102, 1987
A; Title: Primary structure of the biotin-binding site of chaptaile: Primary structure of the biotin-binding site of chaptaces on manager and an acetyl-CoA carboxylase; 493-820 and a2933
A; Molecule type: mRNA
A; Residues: 493-820 and an acetyl-CoA carboxylase; biotin carboxylase
C; Superfamily: human acetyl-CoA carboxylase; biotin carboxylase chaptaces biotin biotin carboxylase homology and predict F; 747-819/Domain: lipoyl/biotin-binding homology and predict F; 747-819/Domain: lipoyl/biotin-binding homology and predict F; 747-819/Domain: lipoyl/biotin-binding homology and predict acetyles.
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Pred. No. 6e-118;
81; Mismatches 10
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                                    ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMV
                                                                                                                                                                                                              VFEHMEQCAVKLAKMVGYVSAGTVEYLYS-QDRSFYFLELNPRLQVEHPCTEMV
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138928
acetyl-CoA carboxylase (EC 6.4.1.2), hepatic - human
N;Alternate names: acetyl-Coenzyme A carboxylase
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 0
C;Accession: 138928
R;Abu-Elheiga, L.; Jayakumar, A.; Baldini, A.; Chirala, S.S.; Wak
Proc. Natl. Acad. Sci. U.S.A. 92, 4011-4015, 1995
A;Title: Human acetyl-CoA carboxylase: characterization, molecula
A;Reference number: 138928; MUD:95249602; PMID:7732023
A;Accession: 138928
A;Status: preliminary
A;Molecule type: mRNA
C;Genetics:
A;Genetics:
A;Genet
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Pred. No. 5.2e-118;
79; Mismatches 104;
                                                                                                                 EVPGSPVFVMKLAGQARHLEVQLLADQYGNAI
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Best Local Similarity 63.6%;
Matches 344; Conservative
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Score 1598.5; DB 2;
Pred. No. 7.6e-106;
92; Mismatches 137;
lipoyl/biotin-binding homology
s: biotin (Lys) (covalent) #sta
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larity 53.9%;
Conservative
                                                      / Match 60.4%;
Local Similarity 65.2%;
nes 326; Conservative
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F;615-687/Domain: li
F;654/Binding site:
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probable acetyl-CoA carboxylase (EC 6.4.1.2) HFA1 - yeast (Saccharomyces cerevisiae)
probable acetyl-CoA carboxylase (EC 6.4.1.2) HFA1 - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein YM8261.01c; protein YM8320.06c; protein YMR207c
C;Species: Saccharomyces cervisiae cervisiae
C;Species: Saccharomyces cervisiae
C;Species: Saccharomyces cervisiae
C;Species: Saccharomyces
C;Accession: S55089
Accession: S55089
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  KOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAER
                                                                             TVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQL
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     2123
                                        11;
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C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-
C;Accession: T07923
R;Schulte, W.; Toepfer, R.; Stracke, R.; Schell, J.; Martini, N.
Proc. Natl. Acad. Sci. U.S.A. 94, 3465-3470, 1997
A;Title: Multi-functional acetyl-coenzyme A carboxylase from Brassi A;Title: Multi-functional acetyl-coenzyme A carboxylase from Brassi A;Title: Multi-functional acetyl-offerences: UNIPROT:004849; UNIPARC:UPI0000A13BD; EMBL:Y10 A;Molecule type: DNA
A;Residues: 1-640 <SCH>
A;Cross-references: UNIPROT:004849; UNIPARC:UPI0000A13BD; EMBL:Y10 A;Experimental source: cv. Akela
C;Genetics:
A;Introns: 111/3; 180/3; 234/3; 265/3; 297/3; 355/3; 387/1; 449/3; C;Function:
A;Description: catalyzes the ATP-dependent carboxylation of acetyl-A;Pathway: fatty acid biosynthesis
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase hom C;Keywords: cytosol; ligase
F;36-542/Domain: biotin carboxylase homology <BCH>
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   Length
ore 1754.5; DB 2;
ed. No. 3.4e-116;
Mismatches 85;
    Score 1754.5;
Pred. No. 3.4
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carboxylase homology;

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12 IGGNELETAPASPUADFIRKQGGHSVITKVLICNNGTAAVKEIRSTRKAAVETECDEEA1 71 1 1 1 1 1 1 1 1 1	RESULT 13 B86483 C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C; Accession: B6483 C; Date: 02-Mar-2001 #text_change 09-Jul-2004 C; Ring, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. anture 408, 816-820, 2000 A; Din, C.W.; Study, D.; Sedano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Mu, D.; Yu, G.; Schwartz, J.R.; Shinn, P.; Southkick, A.W.; Sun, H.; Tallon ker, M.; Mu, D.; Yu, G.; Exaser, C.M.; Venter, J.C.; Davis, R.W. A; Anthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southkick, A.W.; Sun, H.; Tallon ker, M.; Mu, D.; Yu, G.; Exaser, C.M.; Venter, J.C.; Davis, R.W. A; Residues: 12-2359 A; Residues: 12-2359 A; Residues: 12-2359 A; Cross-references: UNIPROT:09C8G0; UNIPARC:UPI0000048337; GB:AE005172; NID:g10645483; C; Generica: A; Map position: 1 C; Superfamily: human acctyl-CoA carboxylase; biotin carboxylase homology; lipoyl/bioti: Query Match Bact Local Similarity S3.3%; Pred. No. 8.4e-104; Matches 305; Conservative 95; Mismatches 137; Indels 35; Gaps Best Local Similarity S3.3%; Pred. No. 8.4e-104; Matches 305; Conservative 95; Mismatches 137; Indels 85; Gaps Cy 12 IGGNPLETAPASPVADFIRKQGGHSVITKVLICHNGIAAVKEIRSIRKMAYETFGDE 68
	RESULT 12 probable acetyl-CoA carboxylase (EC 6.4.1.2) - rape C;Species: Brassita napus (rape) C;Species: Brassita napus (rape) C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004 C;Accession: T0793-0 C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004 C;Accession: T0793-0 Biac Physiol: 106, 793-794, 1994 A;Title: A gene encoding acetyl-coenzyme A carboxylase from Brassica napus. A;Reference number: Z1617; MUID:95083764; PMID:7991694 A;Title: A gene encoding acetyl-coenzyme A carboxylase from Brassica napus. A;Rolecule type: DNA; A;Rolecule type: DNA; A;Rolecule type: DNA; A;Residues: 1-2304 «SCH» A;Residues: 1-2304 «SCH» A;Residues: 1-2304 «SCH» A;Residues: 1-2304 (SCH) A;Rolecules: 100/1; 213/3; 228/3; 336/3; 367/3; 399/3; 457/3; 489/1; 548/3; 565/3; 579/1; A;Rolecules: 100/1; 213/3; 1578/3; 2286/3 A;Introns: 100/1; 213/3; 1578/3; 280/3; 367/3; 489/1; 548/3; 565/3; 579/1; A;Bentics: Bent Local Similarity A;Conservative 105; Mismatches 146; Indels 4; Gaps 2;

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Rishorrosh, B.S.; Dixon, R.A.; Ohlrogge, J.B.

Proc. Natl. Acad. Sci. U.S.A. 91, 4323-4327, 1994

A;Title: Molecular cloning, characterization, and elicitation of acetyl-CoA carboxylas:

A;Title: Molecular cloning, MuID:94240129; PMID:7910406

A;Reference number: Ass381; MuID:94240129; PMID:7910406

A;Reference number: Ass381; MuID:94240129; PMID:7910406

A;Residues: 1-257 csHO

A;Residues: 1-2257 csHO

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C;Generical

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C;Keywords: ligase

F;41-547/Domain: biotin carboxylase homology cbH>

F;674-746/Domain: lipoyl/biotin-binding homology clbB>
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                     TFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVH
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protein F5J5.19 [Imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Accession: D86483

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.B.; Coway, T.H. ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: D86483

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: UNIPROT:Q9SKV1; UNIPARC:UPI0000A0B33; GB:AE005172; NID:C;Genetics:

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A;Genetics:
A;Genetics:
A;Map position: 1

C;Superfamily: human acetyl-CoA carboxvlase: biotin carbovulase
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larity 53.5%; Pred. No. 1.2e-103;
Conservative 96; Mismatches 143;
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A;Introns: 69/1; 90/2; 209/3; 278/3; 332/3; 363/3; 395/3; 453/3; 485/1; 547/3; 564/3; C;Function: A;Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA A;Pathway: fatty acid biosynthesis C;Superfamily: human acetyl-CoA carboxylase, biotin carboxylase homology; lipoyl/biotic; C;Keywords: ligase F;134-640/Domain: biotin carboxylase homology <bch> F;134-640/Domain: lipoyl/biotin-binding homology <lpb> F;767-839/Domain: lipoyl/biotin-binding homology <lpb> F;767-839/Domain: lipoyl/biotin-binding homology <lpb> F;806/Binding site: biotin (Lys) (covalent) #status predicted Query Match Best Local Similarity 54.0%; Pred. No. 5.8e-103; Matches 297; Conservative 95; Mismatches 137; Indels 21; Gaps 5;</lpb></lpb></lpb></bch>	VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATP 79		QY 377 IPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQ 429 :	Oy 550 AERPPADLAV 559 ::	A57710 acetyl-CoA carboxylase (EC 6.4:1.2) - wheat c.Species: Triticum aestivum (common wheat) C;Species: Triticum aestivum (common wheat) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A57710 R;Gornicki, P.; Podkowinski, J.; Scappino, L.A.; DiMaio, J.; Ward, E.; Haselkorn, R. Proc. Natl. Acad. Sci. U.S.A. 91, 6860-6864, 1994 A;Title: Wheat acetyl-Coenzyme A carboxylase: cDNA and protein structure. A;Reference number: A57710: MUID: 94316597: PMID: 7913745	Q41511; UNIPARC:UPI00000 CoA carboxylase; biotin oxylase homology <bch></bch>
	320 RESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPA 3 1.	QY 491 GADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTA 550	acetyl-CoA carboxylase (EC 6.4.1.2) - wheat N;Alternate names: acetyl-coenzyme A carboxylase C;Species: Triticum aestivum (common wheat) C;Date: 05-Nov-1999 #sequence revision 05-Nov-1999 #text_change 09-Jul-2004 C;Accession: T06161; T06162; 542660; S78600; S35959 R;Gornicki, P.; Faris, J.; Podkowinski, J.; Gill, B.; Haselkorn, R. Proc. Natl. Acad. Sci. U.S.A. 94, 14179-14184, 1997 A;Title: Plastid localized acetyl-CoA carboxylase of bread wheat is encoded by a single A;Reference number: 215495; MUID:98054381; PMID:9391173 A;Accession: T06161 A;Status: preliminary; translated from GB/EMBL/DDBJ	A; Residues: 1-2311 <gor1> A; Residues: 1-2311 <gor1> A; Cross-references: UNIPROT: 048959; UNIPARC: UPI00000A9808; EMBL: AF029895; NID: g2827149; A; Experimental source: cv. Hard Red Winter Tam 107, light-grown seedlings A; Accession: T06162 A; Accession: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA</gor1></gor1>	A; Residues: 1-10, 'F', 12-67, 'H', 69-502, 'T', 504-619 <gor2> A; Cross-references: UNIPARC: UPI00000A5F07; EMBL: AF029897; NID: 92827153; PIDN: AAC39332.1; A; Experimental source: cv. Hard Red Winter Tam 107, light-grown seedling R; Elborough, K.M.; Simon, J.W.; Swinhoe, R.; Ashton, A.R.; Slabas, A.R. Plant Mol. Biol. 24, 21-34, 1994 A; Title: Studies on wheat acetyl CoA carboxylase and the cloning of a partial cDNA. A; Reference number: S42660; MUID: 94154234; PMID: 7906561 A; Accession: S42660 A; Molecule type: mRNA</gor2>	A; Residues: 'WRTYM', 1771-2026, 'K', 2028-2073, 'F', 2075-2108, 'V', 2110-2120, 'L', 2122, 'A', 212 A; Cross-references: UNIPARC: UP100000ABB05; EMBL: Z23038; NID: 9396278; PIDN: CAA80573.1; PI A; Accession: S78600 A; Molecule type: protein A; Residues: 1847-1852, 'E', 1854-1863; 1947-1962, 'D', 1964; 2085-2091, 'HL', 2139-2155, 'I', 2157 A; Cross-references: UNIPARC: UP100001552CB; UNIPARC: UP100001552CD; UNIPARC: UP1000017627F; C; Genetics: Acc-1

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C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T07081
R;Anderson, J.V.; Storey, K.; Plaisance, K.; Gengenbach, B.G.; Gronwald, J.W.
impublished results 1996, cited by EMBL
A;Reference number: Z15904
A;Reference number: Z15904
A;Accession: T07081
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A;Accession: T07081
A;Accession: J07081
A;Accession: J07081
A;Accession: J07081
A;Cross-references: UNIPROT:Q39849; UNIPARC:UPI00000A024A; EMBL:L48995; NID:gl066856
A;Experimental source: strain Williams 82; leaf
                                                                                             malonyl
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                                                                                                                              carboxylase homology;
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                                                                                             to
                                        471/
                                                                                                                                                                                                                                          2261
                                                                                                                                                                                                                                                                              15;
                                         454/3;
C;Genetics:
A;Gene: ACCase-A
A;Introns: 116/3; 185/3; 239/3; 270/3; 302/3; 360/3; 391/3; 454/3
A;Introns: 116/3; 185/3; 2243/3
5/3; 1466/3; 1525/3; 2243/3
C;Function:
A;Description: catalyzes the ATP-dependent carboxylation of acety
A;Pathway: fatty acid biosynthesis
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase h
C;Keywords: ligase
C;Keywords: ligase
F;41-547/Domain: biotin carboxylase homology <BCH>
F;41-547/Domain: biotin carboxylase homology <BCH>
F;713/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                      Score 1558.5; DB 2;
Pred. No. 3.4e-102;
; Mismatches 141;
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Local Similarity 53.6%;
nes 293; Conservative
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A;Residues: 941-986,'N',988-1356,'P',1358-1458,'T',1460-1650,'P',1652-1781,'V',1783-1857
A;Cross-references: UNIPARC:UPI00000A836B; EMBL:L49020; NID:g1066858; PIDN:AAA81579.1; A
A;Experimental source: cultivar Lambe rt; leaf
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C; Species: Glycine max (soybean)
C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-C; Accession: T07084; T07083
R; Anderson, J.V.; Lutz, S.M.; Gengenbach, B.G.; Gronwald, J.W.
Plant Physiol. 109, 338, 1995
A; Title: Genomic sequence for a nuclear gene encoding acetyl-coenzyme a A; Reference number: Z15907
A; Reference number: Z15907
A; Reference number: L1008
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-2261 <LIU>A; Coss-references: UNIPROT: Q42793; UNIPARC: UPI00000A76CA; EMBL: L42814; A; Experimental source: strain Williams 82; leaf
R; Anderson, J.V.; Storey, K.; Plaisance, K.L.; Gengenbach, B.G.; Gronwa unpublished results 1996, cited by EMBL
A; Reference number: Z15906
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                                                                                            Indels
  F;661-733/Domain: lipoyl/biotin-binding homology <LPB>F;700/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                             132;
                                                        Score 1565; DB 1;
Pred. No. 1.2e-102
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Mismatches
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                                             to
                                                                             carboxylase homology;
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A48757
acetyl-CoA carboxylase (EC 6.4.1.2) - Cyclotella cryptica
C; Species: Cyclotella cryptica
C; Species: Cyclotella cryptica
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-C; Accession: A48757
R; Roessler, P.G.; Ohlrogge, J.B.
J. Biol. Chem. 268, 19254-19259, 1993
A; Title: Cloning and characterization of the gene that encodes acet A; Reference number: A48757; MUID: 93374903; PMID: 8103514
A; Accession: A48757
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-2089 <ROE>
A; Cross-references: UNIPROT: 039478; UNIPARC: UPI00000A5A26; GB: L2078
A; Cross-references: UNIPROT: 039478; UNIPARC: UPI00000A5A26; GB: L2078
A; Note: authors translated the codon GGC for residue 1834 as Ala
C; Genetics:
A; Introns: 25/1; 729/1
C; Superfamily: human acetyl-CoA carboxylase; biotin carboxylase home
                                                                                                                                                                      Length
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                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFD-----
                                           carboxylation
      A; Experimental source: strain acco, ----
C; Function:
A; Description: catalyzes the ATP-dependent carboxylation
A; Description: catalyzes the ATP-dependent carboxylation
A; Pathway: fatty acid biosynthesis
C; Superfamily: human acetyl-CoA carboxylase; biotin caco; Keywords: ligase
C; Keywords: ligase
F; 134-640/Domain: biotin carboxylase homology <BCH>F; 134-640/Domain: lipoyl/biotin-binding homology <LPB>
                                                                                                                                                                 53.1%; Score 1543.5; DB 2 larity 53.5%; Pred. No. 4.2e-101; Conservative 94; Mismatches 141;
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AERPPWYISV
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                                          526/3
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                                                                                            malonyl-CoA
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                                                                                                                              biotin carboxylase homology;
                                                                                                                                                                                                                                                          Gapa
                                          71/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetyl-CoA carboxylase (EC 6.4.1.2) - maize
N; Alternate names: acetyl-coenzyme A carboxylase
N; Alternate names: acetyl-coenzyme A carboxylase
C; Species: Zea mays (maize)
C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2
C; Accession: T02235
R; Egli, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.
R; Egli, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.
R; Egli, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.
R; Egli, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.
R; Egli, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.
R; Egli, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.
R; Egli, M.A.; Lutz, S.M.; Somers, D.A.; Gengenbach, B.G.
R; Fitle: A maize acetyl-coenzyme A carboxylase cDNA sequence.
A; Reference number: Z14632; MUID: 95357420; PMID: 7630949
A; Accession: T02235
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-2325 < EGL>
A; Cross-references: UNIPROT: Q41743; UNIPARC: UPI00000A4B72; EMBL: U19183;
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                                          454/3;
                                                                                           acetyl-CoA
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                                        391/3;
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                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                 ch 53.5%; Score 1555.5; DB 2 1 Similarity 53.2%; Pred. No. 4.6e-102; 291; Conservative 100; Mismatches 141;
                                      360/3;
                                                                                            carboxylation
C;Genetics:
A;Gene: ACCase-B
A;Introns: 116/3; 185/3; 239/3; 270/3; 302/3; 360/3; 5/3; 1464/3; 1524/3
C;Function:
A;Description: catalyzes ATP-dependent carboxylation
A;Pathway: fatty acid biosynthesis
C;Superfamily: human acetyl-CoA carboxylase; biotin
C;Keywords: ligase
F;41-547/Domain: biotin carboxylase homology <BCH>F;674-746/Domain: lipoyl/biotin-binding homology <LF
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                                38;
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                                                                                        PDIRTI--VVSGNSLTNDAADQYESMEQFIHSHVADIEKRR
  DB 2;
.6e-85;
.es 161;
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38.6%; Score 1121; DB 2;
Best Local Similarity 42.7%; Pred. No. 3.1e-71;
Matches 227; Conservative 97; Mismatches 175;
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  Score 1314; Di
Pred. No. 7.6e
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T28F3.5 - Caenorhabd C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15 C; Accession: T25421
R; Mortimore, B.
submitted to the EMBL Data Library, Novem A; Reference number: Z20032
A; Accession: T25421
A; Status: preliminary; translated from GBA; Molecule type: DNA
A; Residues: 1-1657 < WIL>
A; Experimental source: clone T28F3
C; Genetics:
A; Gene: CESP: T28F3.5
A; Map position: 4
A; Introns: 32/3; 79/1; 153/1; 248/3; 314/
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                               84;
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Conservative
   Query Match
Best Local Similarity
Matches 276; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable acetyl-CoA carboxylase (EC 6.4.1.2) W09B6.1 [similarity] - C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-C;Accession: T32413
R;Goela, D.; Maggi, L.; Andrews, S.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid W09B6.
A;Reference number: 221162
A;Residues: 1-2054 <GOE>
A;Residues: 1-2054 <GOE>
A;Residues: 1-2054 <GOE>
A;Cross-references: UNIPROT: Q9GZI3; UNIPARC: UPI0000075897; EMBL: AF0
A;Experimental source: strain Bristol N2; clone W09B6
C;Genetics:
A;Gene: CESP:W09B6.1
A;Map position: 2
A;Introns: 18/3; 50/3; 97/1; 734/2; 793/3; 1975/2; 2037/2
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase hom
C;Keywords: ligase
                                                                            2089
                                                                                                                                                                                                                                                                                                                                                                                                                                                        [similarity]
                                                                          Length
                                                                                                        Indels
C;Keywords: biotin binding; ligase
F;99-603/Domain: biotin carboxylase homology <BCH>
F;731-803/Domain: lipoyl/biotin-binding homology <LPB>
F;770/Binding site: biotin (Lys) (covalent) #status predicte
                                                                                                                                                                                                                                                       LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGT-
                                                                        DB 1;
                                                                        Score 1502.5; DB 1
Pred. No. 3e-98;
5; Mismatches 140;
                                                                                                     95;
                                                                        ch 51.7%;
1 Similarity 53.2%;
291; Conservative
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| Oy 192 MSDOGFLTVSDDVYQQACHTAREGLEKARKIGYPVMIKASEGGGGKGIRKCTNGEFKQ 251 Db 286 PPGSSWTIPETANASCQYVGYPAMIKASEGGGGKGIRKCTNGEFKQ 251 S1 ::: : :: :: :: Db 285 LINAVLGEVPGSPVFWKLAGQARHI 277 A69123 A69124 Bictin carboxylase - Methanobacterium thermoautotrophicum (strain Delta H) C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 Reguence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: A69127 R; Vicaire, R; Wang, Y; Wierzbowski, J; Aldredge, T. C;Date: 05-Dec-1997 R;Smith, DR.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T. R;Smith, DR.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T. R;Smith, DR.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Riwani, K.; S; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A;Title: Complete ganome sequence of Methanobacterium thermoautotrophicum Delta H: fun A;Reference number: A69000; MUID:98037514; PMID:9371463 A;Status: prellminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Rejachuse; Prellminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Rejachuse; Prellminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Rejachuse; Prellminary; nucleic acid sequence not shown; translation not shown C;Genetics: A;Genetics: Query Match 24.94; Score 724; DB 2; Length 491; |
|--|---|
| 99 82 LKVNADYIRMADOYVEVPGGSRNANYANYDLIVDVAERACVHAVWAGWGHASENPRLPES 141 19 | RESULT 24 probable acetyl-CoA carboxylase (EC 6.4.1.2), chloroplast - rape (fragment) Cipsecies: Brassica mapus (rape) Cipsecies: all strassica mapus (rape) Rischersence manuer; Information (rape) Rischersence; UNIPPOT: O04850; UNIPARC: UPI000009F1F2; EMBL: Y10302; PIDN: CAA71347.1 Rischersence; UNIPPOT: O04850; UNIPARC: UPI000009F1F2; EMBL: Y10302; PIDN: CAA71347.1 Cigenetics: UNIPPOT: O13/3; 386/3; |

strain

PIDI

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S.R.; More
Rajandrea
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M.A.;
     Anabaena
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--RGHAIECRINAEDPDHDFRPAPGRIS-
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C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-;
C; Accession: H81978
R; Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; F; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, N Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria meni A; Reference number: A81775; MUID:2022556; PMID:10761919
A; Accession: H81978
A; Molecule type: DNA
A; Residues: 1-453 < PAR>
A; Cross references: UNIPROT:09JW07; UNIPARC:UPI00000C49E5; GB:AL162753; A; Experimental source: serogroup A, strain Z2491
C; Genetics:
A; Gene: accC; NMA0596
C; Superfamily: blotin neighbored.
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Quail,
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   of
                                                                                                                                                                                                                                                            93;
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    coenzyme A carboxylase PMID:8102363
A; Title: Genes for two subunits of acetyl coenzyme A carboxylar A; Reference number: A53311; MUID: 93352435; PMID: 8102363 A; Accession: A53311 A; Accession: A53311 A; Accession: A53311 A; Accession: A53311 A; Accession: A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-447 < GOR> A; Residues: 1-447 < GOR> A; Cross-references: UNIPROT: Q06862; UNIPARC: UPI00001251AA; GB: C; Superfamily: biotin carboxylase; biotin carboxylase homology C; Keywords: ATP; ligase F; 5-447/Domain: biotin carboxylase homology < BCH>
                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                               Similarity 32.9%; Score 709.5; Di Similarity 32.9%; Pred. No. 9e-43; 0; Conservative 88; Mismatches 1
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                                                                    C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Note: Nostoc sp. BCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Note: Nostoc sp. etrain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Note: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Bacesion: AH1923
R;Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Residues: 1-447 <KUR>
A;Molecule type: DNA
A;Residues: 1-447 <KUR>
A;Cross-references: UNIPROT:006862; UNIPARC:UPI0001251AA; GB:BA000019; PIDN:BAB72896.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: accC
C;Superfamily: biotin carboxylase; biotin carboxylase homology
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A53311
biotin carboxylase (EC 6.3.4.14) - Anabaena sp. (strain PCC 7120)
N;Alternate names: acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxylase C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004 C;Accession: A53311
R;Gornicki, P.; Scappino, L.A.; Haselkorn, R.
J. Bacteriol. 175, 5268-5272, 1993
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DEAVCIG
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|----DRNALHVQLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               24.4%; Score 709.5; DB 2; larity 32.9%; Pred. No. 9e-43; Conservative 88; Mismatches 165.
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Best Local Similarity
Matches 170; Conser
                                                            carboxylase
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ligase

C, Keywords:

carboxylase N <BCH>

carboxylase;

biotin c : biotin

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C; Superfamily: F; 4-450/Domain
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C;Species: Bacillus subtilis
C;Accession: A69581
C;Accession: A69581
C;Bernaria, R;Burlach, S;Bernaria, R;R;Bernaria, R;R;Bernaria, R;R;Bernaria, R;R;Bernaria, R;R;Bernaria, S;Bernaria, R;R;Bernaria, S;Bernaria, R;R;Bernaria, S;Bernaria, R;R;Bernaria, R;R;Reger, M;R;Reger, M;Reger, M;
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                                                                                                                                                                                                                                                                                                                                              ---DGALPDDG-
                                    DB 2;
                                                                              Mismatches
                                      Score 679;
Pred. No.
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1 MLKKVLIANRGEIALRVLRACREMGIAT-
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                              23.4%;
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                                                 al Similarity
170; Conserv
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biotin carboxylase (acc) homolog - Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: D69277
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dods.
r; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archany Rittle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archany Rittle: D69277
A; Mccession: D69277
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: UNA
A; Molecule type: Uniparcing card sequence not shown; translation not shown
C; Superfamily: biotin carboxylase; biotin carboxylase homology
F; 4-450/Domain: biotin carboxylase homology
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                                                      Score 676; DB Pred. No. 2.2e-1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 VITKVLICNNGIAAVKEIRSIRKWAYETFG---
biotin ca
homology
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                                                     ch 23.3%;
1 Similarity 33.2%;
172; Conservative
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biotin carboxylase (acc)
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Dods.

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us-10-633-835-2.rpr

CSTAKKTMQKSGVPCVPGS	C. C. C. Sanith, D.R. S. A. M. S. Linge, L. S. L.; Moir, D. T.; King, B. L.; Brown, E. D.; Doig, P. C.; Smith, D.R. S. A. M. S. Linge, L. S. L.; Moir, D. T.; Mills, S. D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Natures 397, 176-180, 1939 standard of two unrelated isolates of the human gastric paid, A. Reterace number: A.1800, MUID:99120857, PMID:9928682 A. A. Rossidues in L. S. L.; Morring, D. S. D.; Mills, S. D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. A. A. Rossidues in L. S. D. M. A. Rossidues in L. S. C. M. A. Rossidues: Prefininary A. Rossidues: Prefininary A. Rossidues: L. L. S. C. M. A. Rossidues: L. L. S. C. M. A. Rossidues: L. S. S. M. A. Rossidues: L. S. S. C. M. A. Rossidues: L. L. S. C. M. A. Rossidues: Internet in the control of the carboxylase homology and the carbox homology and the carbox homology and the carb
09 IRMADQYVEVPGGSNNNNYANYDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHK 148 1 1 1 1 1 1 1 1 1	PAGENTY 31 Sydago Diotin carboxylase accC - Synechocystis sp. (strain PCC 6803) Nilternate names: hypothetical protein s110053 Cispecies: Synechocystis sp. Cispe

Qy	<pre>noyl-CoA carboxylase (EC 6.4.1.4 pium meliloti #sequence_revision 24-Aug-2001 # ar, S.; Wong, K.; Buhrmester, J. t. U.S.A. 98, 9889-9894, 2001</pre>	complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fix number: A95842; MUID:21396508; PMID:11481431 G95929 eliminary ype: DNA 1-662 <kur> rences: UNIPROT:Q92VJ8; UNIPARC:UPI00000CB61A; GB:AL591985; PIDN:CACal source: strain 1021, megaplasmid pSymB F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy ain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fishe S.W.; Jones, T. 668-672, 2001</kur>	A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Ki hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Well A; Title: The composite genome of the legume symbiont Sinorhizo A; Reference number: A96039; MUID:21368234; PMID:11474104 A; Contents: annotation C; Genetics: A; Genetics: A; Gene: mccB; SMb21124 A; Genome: plasmid C; Superfamily: human acetyl-CoA carboxylase; biotin carboxylas C; Keywords: ligase	Query Match 22.9%; Score 666; DB 2; Length 662; Best Local Similarity 33.1%; Pred. No. 2e-39; Matches 176; Conservative 84; Mismatches 195; Indels 76; Gaps 12; Qy 37 VITKVLICHNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYV 96 :: :	OY ST EVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPG 156	OY 217 LEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAG 272 :: :	Qy 333 LVGYVSAGTVEWLXSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGI 388 : 265 AIGYVGAGTVEFIADVTNGLWPDHFYFMEMNTRLQVEHPVTEAITGIDLVEWQLRVASGE 324 Qy 389 PLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKP 448 325 PL
Oy 334 VGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIPAAQLQVAMGIPLYSI 393 :	Oy 454 TELNFRSSTSTWGYFSVGTSGALHEYADSOFGHIFAYGADRSEARKOMVISLKE 507	rboxylase, biotin carboxylase NMB1861 [imported] - Neilseria meningitidis r-2000 #sequence_revision 31-Mar-2000 #text_change 09-181033 .; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelly Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, andi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.	Nete genome sequence of Neisseria meningitidis serogroup B strain MC58 number: A81000; MUID:20175755; PMID:10710307 F81033 Niminary Pe: DNA -453 <tet> -453 <tet> Sences: UNIPROT:09JXW3; UNIPARC:UPI00000C47EE; GB:AE002536; GB:AE002098 Source: serogroup B, strain MC58 Source: serogroup B, strain AC58 Sibitin carboxylase; biotin carboxylase homology</tet></tet>	Similarity 32.4%; 9; Conservative 9: VITKVLICNNGIAAVKEIR; :: :: : MLKKVLIANRGEIALRVLR.	97 EVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPG : : : :	217 LEKAEKIGYPVMIKASEGGGKGIRKCTNGEEFKQLYNAVLGEVPGSP-VFVM	333 LVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPL-Y

Ivanova).; Lete:

C.; Los, T. O'Callaghan,

er, Mujer, 8, S.;

R.J.; Patra, G.; M. zer, P.H.; Hagius,

31-Dec-2004

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01-Feb-2002

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melite

Brucella

intracellular pathogen

lipoyl/bioti

carboxylase homology;

biotin

12

Gaps

91;

Indels

177;

Mismatches

85;

667

Length

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DB

e-39;

660.5; No. 5e-

Score Pred.

96

981

57

PIDN: AAL

GB: AE008917;

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37 VITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYV
                                                                                                                                                                                                               UNIPROT:Q8YHJ8; UNIPARC:UPI0000057E0A;
e: strain 16M
C; Species: Brucella melitensis
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002
C; Accession: AB3352
R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Pat.
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A; Title: The genome sequence of the facultative int
A; Reference number: AD3252; PMID:11756688
A; Accession: AB3352
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-667 < KUR>
A; Cross-references: UNIPROT:QSYHJ8; UNIPARC:UPI000(A; Experimental source: strain 16M
C; Genetics:
A; Gene: BMEI0800
A; Map position: I
C; Superfamily: human acetyl-CoA carboxylase; biotir
C; Keywords: ligase
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C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: B6456
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleis
S;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleis
Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.;
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter IA; Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B6456
A;Status: preliminary; nucleic acid sequence not shown; translation not show A;Residues: 1-458 <TOM>
A;Residues: 1-458 <TOM>
A;Cross-references: UNIPROT:025134; UNIPARC:UPI0000003173; GB:AE000553; GB:A;Cross-references: UNIPROT:025134; UNIPARC:UPI0000003173; GB:AE000553; GB:A;Cross-references: Uniparcian carboxylase; biotin carboxylase homology <F;18-458/Domain: biotin carboxylase homology <BCH>
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                                                                                       SAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -FRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARK
                                                                EVPGGSNINNIYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPG
                                                                                                                                                                                                - ADEA
                                                                                                                                                                                                                                           PVFVMKLAG
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LEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGS
                                                                                                                                                                                              -GHMGLIED
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-VLLADE
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AQEVNYAGAGTLEFIMD-RDGNYYFMEMNTRIQVEHCVSEMISSLDLVRLQIEIAAGLGL
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                                                                        -GDERAIEFTVMATPEDLKVNADYIRMADQ
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                                                                                                                                                                                                            | | - :: | : | : | : | : | : | : | :| | | SVCVGPPASNQSYLNIPNILSAALMTGAEAIHPGYGFMAENPDFAE--MCREHGIVFIGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- EKAGVVFIGPPV
                                                                                                                                                                                                                                                                                                                                                                                   --GSPVFVM-KL
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Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein AGR_L_580GM [imported] - Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 31-D C; Accession: F98286 R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; O A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lapp Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agel A; A; Eterence number: A97359; MUID:21608551; PMID:11743194
A; Reference number: A97359; MUID:21608551; PMID:11743194
A; Residues: 1-667 < KUR>
A; Residues: 1-667 < KUR>
A; Residues: 1-667 < KUR>
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: human acetv1-CoA control of action: linear chromosome
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Pred. No. 9.6e-39;
95; Mismatches 185;
                                                                                                      TPESMRALGSKAGGREIAAQSNVPTVP--GTGVLESV
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1 MIKKILIANRGEIACRVIKTAKKMGIAT
                                                                           40 KVLICNNGIAAVKEIRSIRKWAYETF--
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170; Conservative
                             Conservative
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    Best Local Similarity
Matches 160; Conser
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Best Local S
Matches 170
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C.; Ma
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T.; Zalewski,
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                                                      GB: AP001
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Superfamily: biotin carboxylase; biotin carboxylase homology
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A;Title: Genome sequence of the radioresistant bacterium Deinc A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B7558
A;Accession: B7558
A;Accession: B7558
A;Accession: B7558
A;Cross: preliminary
A;Molecule type: DNA
A;Residues: 1-445 < WHI>
A;Cross-references: UNIPROT:Q9RY34; UNIPARC:UPI00000D3C48; GB:A;Experimental source: strain R1
C;Genetics:
A;Genetics:
A;G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEFEVEG-IETTIPFHLRLLNHETFVSGDFNTKFLE
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                                                                                                                                                                                                  Score 660; DB 2
Pred. No. 3e-39;
12; Mismatches 1
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LKSYLAPGGLGVRVDSAAYPGY
A; Molecule type: DNA
A; Residues: 1-452 <STO>
A; Cross-references: UNIPROT: Q9K963;
A; Experimental source: strain C-125
C; Genetics:
A; Gene: accC
C; Superfamily: biotin carboxylase; b
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larity 32.8%;
Conservative 8
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B.; Goldm Markelz,

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PIDN: AAK89816

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PPWIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGS----PVFVMKLAG 272
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                                                            3MD PRGNEVI DFDFSSPESFKTQRKPQPQGHVVACRI TAENPDTGFKPGMGA
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version
- 2006
GenCore
(c) 1993
        Copyright
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US-10-633-835-2 2907 1 PPPDHKAVSQFIGGNPLETA.. Title: Perfect

score: Sequence:

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residues 0.5 82675679 Gapext seds, 572060 Searched:

572060 hits satisfying chosen parameters of Total number

2000000000 length: length: seq seq 08 Minimum Maximum

Post-processing:

summaries Minimum Match 0% Maximum Match 100% Listing first 45 st

Patents Issued

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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:* 4 0 m 4 m v

to have a being printed Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being p and is derived by analysis of the total score distribution.

SUMMARIES

cript	equence 3, Appl	equence 120 equence 1,	equence 119, Ap	equence 118,	equence 3, Appl	equence 3, Appl	equence 8, Appl	equence 17027,	quence 10, App	equence 10, App	equence 10, App	equence 9, Appl	equence 6, Appl	equence 6, App	e 6, Appl	equence 6, App	equence 1	Sequence 23, Appl	equence 24, Ap	equence 31, App	equence 74, App	76, App	e 2, A	9, Ap	equence 109,	9, Ap
Ω	US-09-581	08-354-973-1	-433-043B-	-09-433-043B-11	-08-677-01	-08-790-519-	-09-839-477-8	-09-248-796A-	-08-611-107-1	-422-56	-08-468-793-1	-08-934-386-	-08-417-08	-08-695-651-	-930-285-	-08-695-421-	-697-826A-1	-08-418-893D-	-08-418-893D-2	-611-	US-09-631-594-74	-631-59	US-09-475-252-2	00B-1	6-537-1	US-08-485-607-109
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Sequence 109, App Sequence 117, App Sequence 117, App Sequence 6, Appli Sequence 6, Appli Sequence 122, App Sequence 8, Appli Sequence 6, Appli Sequence 6725, Appli Sequence 6725, Appli Sequence 17494, A													
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US-08-475-879-109 US-09-433-043B-109 US-09-433-043B-117 US-08-611-107-6 US-08-468-793-6 US-09-433-043B-122 US-09-433-043B-122 US-08-468-793-8 US-08-468-793-8 US-08-468-793-8 US-08-476-537-6 US-08-485-607-6 US-08-485-607-6 US-09-433-043B-121 US-09-433-043B-121 US-09-328-352-6725 US-09-248-796A-17494	•												
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ALIGNMENTS

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                                              GENERAL INFORMATION:

APPLICANT: Graham Keith DIXON
APPLICANT: John Leslie THAIN
APPLICANT: John Philip VINCENT
APPLICANT: John Philip VINCENT
APPLICANT: John Philip VINCENT
APPLICANT: Suberna Jini CHAVDA
TITLE OF INVENTION: Acetyl-CoA-Carboxylase from Candida Albicans
FILE REFERENCE: 009901/0270671 - PJF/PHM70303/UST
CURRENT APPLICATION NUMBER: US/09/581,909
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: PCT/GB98/03857
PRIOR APPLICATION NUMBER: GB 9726897.3
PRIOR APPLICATION NUMBER: GB 9726897.3
PRIOR SEQ ID NOS: 3
SEQ ID NO 3
LENGTH: 2270
TYPE: PRT

CORGANISM: Candida albicans
US-09-581-909-3
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2-179;
98;
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Pred. No. 2e-1
63; Mismatches
Sequence 3, Application US/09581909
Patent No. 6566048
GENERAL INFORMATION:
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Best Local Similarity 70.7%; Pr
Matches 390; Conservative 63;
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308 EEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHP

310 NFITLYNQAANEIPGSPIFIMKLAGDARHLEVQLLADQYGTNISLFGRDCSVQRRHQKII

EFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKII

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HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPW
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                              DSOFGHIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL
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Pred. No. 2.7e
6; Mismatches
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520 White Plains
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                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08354973
Patent No. 5641666
GENERAL INFORMATION:
APPLICANT: Vahlensieck, Hans-Friedrich
APPLICANT: Hinnen, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/354,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STALL.
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
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3R: PF/
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TELEPHONE: 919-541-8582
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NAME: Pace, Gary
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                         Fungi
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TITLE OF INVENTION: Fung
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Patent Dept.,
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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FILING DATE: 13-DE
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386; Conserv
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ATTORNEY/AGENT IN
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                                             TTEMVSGVNI PAAQLQVAMGI PLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQ
                                                            29 PGH-----FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAVKEIRSVRKWAY
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                                                                                                     SOFGHI
                                                                                                                       GGGGKGI
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLA FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2.1
                                                                                                   POGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYAL
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370- EEAPVTIARKETFHEMENAAVRLGKLVGYVSAGTVEYLYSHAEDKFYFLELNP
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Best Local Similarity 69.1%; Pred. No. 5.46
Matches 386; Conservative 76; Mismatches
                                                                                                                                                                                                                                                                                                                            Sequence 120, Application US/094330431
Patent No. 6399342
GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                       621
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LENGTH: 802
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Pred. No. 6.5e-153;
; Mismatches 104;
                                                                                                                                                                       of Artificial
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TITLE OF INVENTION: CYANOBACTERIAL AND
FILE REFERENCE: ARCD:338US
                                                                                                                                                                                                                                                                                                                                                                                 US-09-433-043B-118; Application US/09433043B; Patent No. 6399342; GENERAL INFORMATION:
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APPLICANT: HASELKORN, ROBERT
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TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2.1
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Patent No. 6399342
GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
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Best Local Similarity
Matches 343; Conser
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                                        -GPGINYETVSQVDEFCKALRGKRPIHSILIANNGMAAVKFIRSVRTWAYE
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MENTION: Structure and Expression
MENTION: Arabidopsis Acetyl-coenzy
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Patentin Release #1.0,
CATION DATA:
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US/08/790,51
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Hills
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ADDRESSEE: Harness, Di
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: Michigan
    Conservative
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; Sequence 3, r.,
; Patent No. 5962767
; GENERAL INFORMATION:
, PPLICANT: Ohlrogge, J
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TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/677,010

FILING DATE:

CLASSIFICATION: 800
                                                                                                                                            Ohlrogge, John B.
Roesler, Keith R.
Shorrosh, Basil S.
VENTION: Structure and Expression of VENTION: Arabidopsis Acetyl-coenzyme
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pierce,
                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08677010 Patent No. 5925805 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 6:
TELECOMMUNICATION INFORMATION
TELEPHONE: (810)641-1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Harness, Did
: P.O. Box 828
Bloomfield Hills
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TITLE OF INVENTION: Ar
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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Sequence 8, Application US/09839477
Patent No. 6723895
GENERAL INFORMATION:
APPLICANT: Shorrosh, Basil S.
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS CONTAINING A CYTOSOLIC ACETYL
TITLE OF INVENTION: COA-CARBOXYLASE
FILE REFERENCE: 07148-094001
CURRENT APPLICATION NUMBER: US/09/839,477
CURRENT FILING DATE: 2001-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGN-
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4.8e-135;
ches 143;
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larity 53.3%; Pred. No. 4.
Conservative 97; Mismatche
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                      REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 655
FELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
                                                                                                                                                                                                                                   , 76
 INFORMATION:
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                                                                          TELEFAX: (810)641-027
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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ATTORNEY/AGENT INFORMAT
NAME: Smith, DeAnn F
REGISTRATION NUMBER:
                                                                                                                                                        unknown
                                                                                                                              amino acid
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Best Local Similarity
Matches 301; Conser
                                                    TELECOMMUNICATION
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; MOLECULE TYPE:
US-08-790-519-3
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Pred. No. 5.3e-135;
93; Mismatches 139;
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US-09-248-796A-17027

; Sequence 17027, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:
    APPLICANT: Keith Weinstock et al
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACI
    TITLE OF INVENTION: FOR DIAGNOSTICS AND THERY
    FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-08-13

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 17027

: LENGTH: 442
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                                      Version
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows V
SEQ ID NO 8
LENGTH: 2257
TYPE: PRT
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NUCLEIC ACID COMPOSITIONS E
ACETYL-COA CARBOXYLASE AND
THEREFOR
                                         Score 1569.5;
Pred. No. 2.3e
49; Mismatches
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APPLICATION NUMBER:
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02-OCT-1992
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,107
FILING DATE: Concurrently Herewith
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). Box 4433
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Patent No. 5801233
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: NUCLEIC ACID
TITLE OF INVENTION: ACETYL-COA CA
                                                             49;
                                         ch 54.0%; l Similarity 70.2%; 295; Conservative
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i TYPE: PRTORGANISM: Candida albicansUS-09-248-796A-17027
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TITLE OF INVENTION: ACET
TITLE OF INVENTION: THEN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
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STATE:
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ss 132;
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ACETYL-COA CA
METHODS FOR U
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ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: AR
                                                            TELECOMMUNICATION INFORMATION TELEPHONE: (512) 418-3000
                                                                                HONE: (512) 418-3000

AX: (512) 474-7577

DN FOR SEQ ID NO: 10:

CHARACTERISTICS:
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Patent No. 5910626
GENERAL INFORMATION:
APPLICANT: Haselkorn,
APPLICANT: Gornicki, P
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CORRESPONDENCE ADDRESS:
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Arnold, White
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NAME: Kitchell, Barbara
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acids
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APPLICATION NUMBER: US
FILING DATE: 06-JUN-15
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INFORMATION FOR SEQ ID NO
SEQUENCE CHARACTER
                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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FILING DATE: 30-SE
                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
Matches 300; Conser
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                                                                                                                                                                                                  CITY: Houston STATE: Texas
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US-08-468-793-10
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                                                                                                Version
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                                                                                                                                                                                                                                       ARCD:152/WIM
                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,560A
FILING DATE: 14-APR-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956,700
                                                                                                                                                                    APPLICATION NUMBER: US 07/956,700 FILING DATE: 02-OCT-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                           37,259
                                                                                                                                                                                                            NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARI
                                                                                                                                                                                                                                                                                           10:
                             ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                    2257 amino acids
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512-474-7577
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Houston
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                      COUNTRY:
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Best Local S
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'.5e-134;
les 132;
                                                                             CARBOXYLASE
USE
                                                                                                                                                                                                                                                                   Version
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Pred. No. 7
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APPLICATION NUMBER: US SN 07/956,7
FILING DATE: 02-OCT-1992
CLASSIFICATION: 800
                                                                                                                                   Durkee
                                                                                                                                                                                      America
                                                                                                                                                                                                                                                                                      MBER: US/08/468,793
06-JUN-1995
                                                                                                                                                                                                                                                              Patentin Release #1.0,
US-08-468-793-10
; Sequence 10, Application US/08468793
; Patent No. 6177267
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
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TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
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CHARACTERISTICS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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INFORMATION FOR SEQ ID
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STRANDEDNESS: six
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GENERAL INFORMATION:
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APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: Methods for Detecting Nucleic Acid
TITLE OF INVENTION: Segments Encoding Acetyl-Coa Carbos
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Amino Acid"
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARSB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 amino acida
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Patent No. 6306636
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
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LOCATION: one-of(291, 316,
OTHER INFORMATION: /note=
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CORRESPONDENCE ADDRESS:
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CITY: H
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FILING DATE: 12-AUG-1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Somers, D. A.
APPLICANT: Wyse, D. L.
APPLICANT: Gronwald, J. W.
APPLICANT: Egli, M. A.
APPLICANT: Lutz, S. M.
TITLE OF INVENTION: METHOD FOR PR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE
MEDIUM TYPE: Di
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FILING DATE: 05-APR-1995
APPLICATION NUMBER: 08/014326
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
FILING DATE: 21-JUL-1992
APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: WOESENEY, WAITEN D
REGISTRATION NUMBER: 600.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
TELEPHONE: 612-339-3061
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US-08-930-285-6
; Sequence 6, Application US/08930285
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N-terminal
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                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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AERPPWYISV
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FRAGMENT TYPE:
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INFORMATION FOR
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Best Local S
Matches 294
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FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
FILING DATE: 21-JUL-1992
APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
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23-AUG-1996
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9, 6268550
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TELEPHONE: 612-373-6900
TELEFAX: 612-339-3061
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N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRENT APPLICATION DATA APPLICATION NUMBER: U
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TITLE OF INVENTION: FO
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   800
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Lutz, S.
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STRANDEDNESS: sin
TOPOLOGY: linear
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OPERATING SYSTEM:
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Patent No. 6268550
GENERAL INFORMATION
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FRAGMENT TYPE:
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                                           of the University of Minnesota, et al TRANSGENIC PLANTS EXPRESSING ACETYL
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                                                                                  NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner
STREET: P. O. Box 2938
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US96/04625
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Embretson, Janet E.
REGISTRATION NUMBER: 39,665
REFERENCE/DOCKET NUMBER: 600.318US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-3061
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R: 600.318US4
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FILING DATE: 13-APR-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                   Version 1.5
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SEQUENCE CHARACTERISTICS:
LENGTH: 2325 amino acids
                                                                                                                                                                                                                                                                                               3: Diskette
IBM Compatible
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                                        APPLICANT: Regents
TITLE OF INVENTION:
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SOFTWARE: FastSE
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GENERAL INFORMATION:
APPLICANT: Regent
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294; Conser
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ORIGINAL SOURCE:
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TOPOLOGY: lir
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Matches 29
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METHODS AND AN ACETYL COA CARBOXYLASE GENE
FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION
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 Score 1543.5; DB 2
Pred. No. 7.4e-132;
; Mismatches 141;
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TOLERANCE IN CORN
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P.O. Box 2938
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US-08-697-826A-10
; Sequence 10, Application US/08697826A
; Patent No. 6414222
                     94;
 53.1%;
llarity 53.5%;
Conservative
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IBM Compatible
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APPLICANT: Gengenbach, B.
APPLICANT: Somers, D. A.
APPLICANT: Egli, M. A.
APPLICANT: Marshall, L. C.
APPLICANT: Wyse, D. L.
APPLICANT: Lutz, S. M.
APPLICANT: Van Dee, K. L.
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L. C.
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CORRESPONDENCE ADDRESS
ADDRESSEE: Schwegman
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Query Match
Best Local Similarity
Matches 294; Conser
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Pred. No. 7.4e-132;
94; Mismatches 141;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
TELEFAX: 612-256
                                 826A
                                                                                                PCT/US96/04625
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,82
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/046
                                                                                                             FILING DATE: 04-APR-1996
APPLICATION NUMBER: 08/679,82
FILING DATE: 30-AUG-1996
ATTORNEY/AGENT INFORMATION:
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Local Similarity 53.5%;
nes, 294; Conservative
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REGISTRATION NUMBER:
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; MOLECULE TYPE:
US-08-697-826A-10
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Best Local S
Matches, 294
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                                           GVNIPAAQLQVAMGIPLYSIRDIRTLYGM-DPRGNEVIDFDFSSPESFKTQRKPQPQGHV
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                                                           | |:|| ||||||||||::| ||| ||| | | : ||| GANLPATQLQVAMGIPLFNIPDIRRLYGREDAYGTDPID
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Pred. No. 3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  RENEWABLE ENERGY
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FILING DATE: April 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/104,938
14, 1993
                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/08418893D
Patent No. 5559220
GENERAL INFORMATION:
APPLICANT: ROESSLER, PAUL G
APPLICANT: OHLROGGE, JOHN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
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REFERENCE/DOCKET NUMBER: MR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-231-1000
TELEFAX: 303-231-1098
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53.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
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NO
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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FILING DATE: Septer
CLASSIFICATION: 80
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TITLE OF INVENTION:
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STRANDEDNESS: sin
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OPERATING SYSTEM:
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Golden
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Best Local Sim:
Matches 291;
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                                                                                 GENE THAT ENCODES ACETYL-COENZYME A CARBOXYLASE FROM CYCLOTELLA CRYPTICA 25
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 3.6e-128;
; Mismatches 140;
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ER: MRI/NREL IR#
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/418,893D
FILING DATE: April 7, 1995
CLASSIFICATION: 800
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per 14, 1993
5-08-418-893D-23
Sequence 23, Application US/08418893D
Patent No. 5559220
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-231-1000
TELEFAX: 303-231-1098
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illarity 53.2%;
Conservative 9
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: O'CONNOR, EDNA
REGISTRATION NUMBER: 29,
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                                                       PAUL
                                                                                                                                                                                                                                                                                                                                                                                       September
                                                   APPLICANT: ROESSLER, PAI
APPLICANT: OHLROGGE, JOH
TITLE OF INVENTION: GENE
TITLE OF INVENTION: CARE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: September
CLASSIFICATION: 800
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US-08-418-893D-23
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APPLICATION NUMBER: US PCT/US93, FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: US SN 08/42: FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION: NAME: Kitchell, Barbara S. REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:23
                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                              HONE: (512) 418-3000
AX: (512) 474-7577
ON FOR SEQ ID NO: 31:
E CHARACTERISTICS:
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US-08-611-107-31
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             ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETF
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Patent No. 5801233
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS E
TITLE OF INVENTION: THEREFOR
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Concurrently Herewith
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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P.O. Box 4433
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CORRESPONDENCE ADDRESS:
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US-08-611-107-31
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CITY: HC
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                                                                               54 IRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLI
                                                                                                                                                                               174 HADVPCMPWSGTGIK---ETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIK
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                                                                                                   Gaps
                                       26;
    Length 2172;
                                         Indels
5; DB 1;
1.9e-127;
ches 121;
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  Score 1495; Di
Pred. No. 1.9e
7; Mismatches
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US-09-631-594-74

Sequence 74, Application US/09631594

Patent No. 6737237

GENERAL INFORMATION:
APPLICANT: MCLEOD, RIMA W.
APPLICANT: ROBERTS, CRAIG W.
APPLICANT: ROBERTS, FIONA
APPLICANT: JOHNSON, JENNIFER J.
APPLICANT: KIRISITS, MICHAEL
APPLICANT: FERGUSON, DAVID
APPLICANT: LYONS, RUSSELL
                                                                                                                                                                                                                                                                         AAGVPTLPWSGSHVKVPQETCHS
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    54.8%;
                  Local Similarity 54.8
hes 284; Conservative
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                                                                  ND VACCINES
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                                             APPLICANT: SUTHER, ELLEN
TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIAGNOSTIC REAGENTS, AN
TITLE OF INVENTION: BASED ON UNIQUE APICOMPLEXAN PARASITE COMPON
FILE REFERENCE: 19338-90966
CURRENT APPLICATION NUMBER: US/09/631,594
CURRENT APPLICATION NUMBER: PCT/US00/11478
PRIOR APPLICATION NUMBER: PCT/US97/12497
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                    40 KVLICHNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMAL
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                                                                                                                                                                                                                                                                                             Score 1417; DB 2;
Pred. No. 2.7e-121;
?; Mismatches 134;
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US-09-631-594-76
; Sequence 76, Application US/09631594
; Patent No. 6737237
; GENERAL INFORMATION:
; APPLICANT: MCLEOD, RIMA.W.
; APPLICANT: ROBERTS, CRAIG W.
; APPLICANT: ROBERTS, FIONA
; APPLICANT: ROBERTS, FIONA
; APPLICANT: JOHNSON, JENNIFER J.
*** TOTAL TOTAL SITS, MICHAEL
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illarity 55.2%;
Conservative 7
             DOUG
L, BENJAMIN
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MUI, ERNEST
MACK, DOUG
SAMUEL, BEI
GORNICKI,
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Best Local Similarity
Matches 277; Conser
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; ORGANISM: TO:
US-09-631-594-74
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           APPLICANT:
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APPLICANT:
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                                                                   APPLICANT: GORNICKI, PIOTR
APPLICANT: ZUTHER, ELLEN
TITLE OF INVENTION: ANTIMICROBIAL AGENTS, DIAGNOSTIC REAGENTS, AND VACCINES
TITLE OF INVENTION: BASED ON UNIQUE APICOMPLEXAN PARASITE COMPONENTS
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                                                                                                                                                                                                                                                                                                                                              Score 1265.5; DB 2
Pred. No. 2.3e-107;
70; Mismatches 143;
                                                                                                         TITLE OF INVENTION: BASED ON UNIQUE APICOMI
FILE REFERENCE: 19338-90966
CURRENT APPLICATION NUMBER: US/09/631,594
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: PCT/US97/12497
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 76
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Patent No. 6514726
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Parkinson, Tanya
Bulawa, Christine
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                                                         BENJAMIN
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             S, RUSSELL
ERNEST
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FERGUSON,
LYONS, RU
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GENERAL INFORMATION:
APPLICANT: Dorr, Pa
APPLICANT: Parkinso
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nes 263; Conser
                          MUI, ERN
MACK, DC
SAMUEL,
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TOPOLOGY: LA MOLECULE TYPE:
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CURRENT APPL
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CITY: C
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  ASPERGILLUS FUMIGATUS ACETYL COENZYME-A CARBOXYLASE
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                                                                                                                                                                                         Length 2016
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NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold
                                                                                                                                                                                                                    Indels
         TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF FILE REFERENCE: 06286/107001
CURRENT APPLICATION NUMBER: US/09/475,252
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US 60/114,580
PRIOR FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                   44;
                                                                                                                                                                                         Score 1152; DB 2;
Pred. No. 5.2e-96;
                                                                                                                                                                                                                 Mismatches
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US/07/956,700B
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NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 109, Application US/07956700B
Patent No. 5539092
GENERAL INFORMATION:
APPLICANT: Robert Haselkorn and Pic
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1 PC Compatible
FEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
FORMATION FOR SEQ ID NO: 109:
                                                                                                                                                   ; ORGANISM: Aspergillus fumigatus US-09-475-252-2
                                                                                                                                                                                          39.6%;
                                                                                                                                                                                                                  Conservative
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APPLICATION NUMBER: US
FILING DATE: 19921002
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM: PO
SOFTWARE: ASCII-DOS
                                                                                                                                                                                                     Local Similarity
hes 221; Conser
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INVENTION:
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US-07-956-700B-109
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                                                                                                                                                                 963.5; DB 1;
No. 1.2e-79;
smatches 89;
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and Plant A
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Cyanobacterial and
Carboxylase
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                                                                                                                          any
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FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5756290thrup
REGISTRATION NUMBER: 33,268
REGISTRATION NUMBER: ARCD:05
                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Floppy Disk
IBM PC Compatible
YSTEM: PC-DOS/MS-DOS
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Patent No. 5756290
GENERAL INFORMATION:
                                                                                                             412
                                                                                                                                                                                                51;
                                                                                  , LOCATION: 248, 267, 311, 4.; IDENTIFICATION METHOD: Xaa
US-07-956-7008-109
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                                                                                                                                                                   33.1%;
                                                                                                                                                                                 Similarity 54.7
37; Conservative
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CHARACTERISTICS
                                       Single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS
ADDRESSEE: Arnold, 1
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APPLICATION DA
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                       Linear
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Chicago
Illinois
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APPLICATION NUMBER:
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Local Similarity
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CITY: C
STATE:
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Best Local
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RGEIRTN
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YGIEHGG
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TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
TITLE OF INVENTION: Carboxylase
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 VDÝTVDĽĽNAAEYRENXÍHTGWĽDSRÍAMRVRAERPPWYĽSV
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                                                                                                                                                                                    33.1%; Score 963.5; DB 1; ilarity 54.7%; Pred. No. 1.2e-79; Conservative 51; Mismatches 89;
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iny amino acid
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Clark Street
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FILING DATE: 07-JUN-1995
                                                                                                                                                     any
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PE: Floppy Disk
IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 5792627
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01/956,700
                                                                                                                                         412,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 109:
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Xaa
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Chicago
Illinois
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                                                      . 491 amino acids
Amino acid
                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                          NAME/KEY: Xaa
LOCATION: 248, 267, 3
IDENTIFICATION METHOD:
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                                                                                Single
                                                                                                     Peptide
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PRIOR APPLICATION DATA:
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                                                                                          Linear
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SOFTWARE: ASCII-
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                                                                            STRANDEDNESS:
                                                                                                     MOLECULE TYPE:
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                                                      LENGTH:
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MENTION: Cyanobacterial and Plant Acetyl-CoA
MENTION: Carboxylase
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                                                                                                                                                                                                                                                                                                                                                                  Score 963.5; DB 1;
Pred. No. 1.2e-79;
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acid
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amino a
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any ar
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5786170th
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                 5792627thrup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Floppy Disk
IBM PC Compatible
YSTEM: PC-DOS/MS-DOS
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                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 109:
                                    33,268
                                                                                                                                                                                                                                                                                        ; LOCATION: 248, 267, 311, 4; IDENTIFICATION METHOD: Xaa US-08-485-607-109
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Chicago
Illinois
INFORMATION
                                                                                                                                                             : 491 amino acids
Amino acid
                                 REGISTRATION NUMBER: 3
REFERENCE/DOCKET NUMBER
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS
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US/08/475,879

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US-09-433-043B-117
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SEQ ID NO 117
LENGTH: 491
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Best Local S
Matches 187
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Best Local S
Matches 187
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                         FEATURE:
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Sequence 109, Application US/09433043B

Patent No. 6399342

GENERAL INFORMATION:
APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B

CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-10-02
PRIOR FILING DATE: 1995-10-02
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33.1%; Score 963.5; DB 1;
Best Local Similarity 54.7%; Pred. No. 1.2e-79;
Matches 187; Conservative 51; Mismatches 89;
                                                                                                                                                                                                                                                                                         418, 422, 436,
any amino acid
                                               FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5972644 5786170thrup.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      422,
                                      MBER: 07/956,700
10/21/92
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                                                                                                                                                                                                                                                               , LOCATION: 248, 267, 311, 4: ; IDENTIFICATION METHOD: Xaa
US-08-475-879-109
07-JUN-1995
                                                                                                                                                                                           amino acids
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SOFTWARE: Patentin Ver. 2
EQ ID NO 109
LENGTH: 491
          CLASSIFICATION: 536
IOR APPLICATION DATA:
                                                                                                                                                                                                                      Single
                                                                                                                                                                                                                                               Peptide
                                    APPLICATION NUMBER:
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Amino acid
                                                                                                                                                                                                                                   Linear
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-09-433-043B-109
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                                       Artificial Sequence
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1.8e-79;
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                                                                                                                                        963.5; DB No. 1.2e-79
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Pred. No. 1.8e
1; Mismatches
                                                                                               containing
                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 117, Application US/09433043B Patent No. 6399342 GENERAL INFORMATION:
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Pred.
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PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEC. 15
                                          of
                                                                                                 set
                                                                                                                                                                   51;
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                                      OTHER INFORMATION: Description OTHER INFORMATION: Peptide NAME/KEY: MOD RES LOCATION: (248)..(474)
OTHER INFORMATION: XAA = Any se-09-433-0438-109
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TYPE: PRT
ORGANISM: Artificial Sequence
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illarity 54.7%;
Conservative 5
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
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187; Conserv
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3-043B-117
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d. No. 2.1e-56;
Mismatches 165
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                                                            LRECAITG-LPTTIGFHORIMENPOFLOGNVSTSFV
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FILING DATE: 14-APR-1995
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FILING DATE: 02-OCT-1992
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08422560A
Patent No. 5910626
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
  Pred
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REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: AR
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              Conservative
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STATE: TX
COUNTRY: USA
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l Similarity
170; Conser
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US-08-422-560A-6
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ACETYL-COA CARBOXYLASE AND USES
THEREFOR
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: 'Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,107
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 08/422 ETLING DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 6, Application US/08611107
Patent No. 5801233
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APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-C
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White &
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                         Robert
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33,
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APPLICANT: Hasel
APPLICANT: Gorni
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CITY: H
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APPLICATION NUMBER: US SN 0'
FILING DATE: 02-OCT-1992
CLASSIFICATION: 800
APPLICATION NUMBER: PCT/US9:
FILING DATE: 30-SEP-1993
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                   CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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            CURRENT APPLICATION DA APPLICATION NUMBER: FILING DATE: 06-JU
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                                                                                                                                          Length
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                                                                                                                               Score 709.5; DB 1;
Pred. No. 2.1e-56;
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| KILIANRGEIALRILRACEEMGIATI----AVHSTV--
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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Gornicki, Piotr
VENTION: ACETYL-COA CAR!
VENTION: METHODS OF USE
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RLMGDKSTAKETMQKAGVPTVPGS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acids
                                                                                                                                                                  88;
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                                                                                                                                       24.4%;
nilarity 32.9%;
Conservative 88
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CORRESPONDENCE ADDRESS:
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APPLICANT: Gornicki,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                     STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                      Query Matcn
Best Local Similarity
Matches 170; Conser
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CITY: H
STATE:
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Version
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Pred. No. 2.
                                                                                                                                                                                                                                                             FILING DATE: 30-SEP-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           PCT/US93/09340
                                                                                                                                 US 08/422,560
                                   MBER: US/08/468,793
06-JUN-1995
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APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
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                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Description of Artificial , OTHER INFORMATION: Peptide US-09-433-0438-122
                                                                                            FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/956,700
PRIOR FILING DATE: 1992-10-02
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Ver. 2.1
             \mathbf{\omega}
          Sequence 122, Application US/094330438
Patent No. 6399342
GENERAL INFORMATION:
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Patent No. 5801233
GENERAL INFORMATION:
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170; Conserv
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ENGTH: 593
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                                                                                                                                                                                                                                           Version
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 08/422,560
FILING DATE: 14-APR-1995
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Pred. No. 8e
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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RAMGDKSTAKETMQRVGVPTIPGS
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BER: 33,928
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ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara
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V FOR SEQ ID NO:
CHARACTERISTICS:
                                                                                                                                             United States
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                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
FILING DATE: Concur
CLASSIFICATION: 800
PRIOR APPLICATION DATA
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                                                                                              P.O. Box
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Rest Local Similarity
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Robert

Haselkorn, Robe Gornicki, Piotr

APPLICANT: PPLICANT:

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HLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVG
                                                               YVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIPAAOLOVAMGIPLYSIRD
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                                                                                                                          CARBOXYLASE COMPOSITIONS USE
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NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
CLASSIFICATION: 800
APPLICATION NUMBER: PCT/US93/09340
FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,793
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
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789-2679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ACTITLE OF INVENTION: MENUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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Patent No. 6177267
GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Texas
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-RQADIQLRGHAIECRINAEDPEYNFRP
                                                                  -GYLPPGGPGVRVDSHVYTDYEIPPYYDSLIGKLIVWGATREEA
                                              -- LHEYADSQFGHIFAYGADRSEA
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                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 8e-54
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USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE: 02-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/horror
                                                                                                                                                                                                                                                                                                                                      ENCE ADDRESS:
E: Arnold, White & Durkee
P.O. Box 4433
                                                                                                                                                                                                                                 APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CAF
TITLE OF INVENTION: METHODS FOR US
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold
                                                                                                                                                                                                                Sequence 8, Application US/08422560A
Patent No. 5910626
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
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TELEPHONE: 512-418-3000
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-APR-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
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US-08-422-560A-8
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STATE: T
COUNTRY:
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US-08-476-537-6; Sequence 6, Application; Patent No. 5756290; GENERAL INFORMATION:
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   TELECOMMUNICATION TELEPHONE: 1-31
                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                   TOPOLOGY: L: MOLECULE TYPE:
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Best Local
Matches 16
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/ENTION: Cyanobacterial and Plant Acetyl-CoA
/ENTION: Carboxylase
                                                                                                                                                                                                                                                                                                                                                             ---DGLLT---DV
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                                                              Score 681.5; DB Pred. No. 8e-54;
                                                                                                     Mismatches
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NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Floppy Disk
IBM PC Compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/07956700B Patent No. 5539092 GENERAL INFORMATION:
                                                                                                     97;
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1 No. 5539092th
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                                                                                                      Conservative
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TITLE OF INVENTION: Car
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA
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168; Conser
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US-08-468-793-8
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US-07-956-700B-6
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ed. No. 1.2e
Mismatches
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TITLE OF INVENTION: Cyanobacterial and
TITLE OF INVENTION: Carboxylase
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n Clark St
                                                                                                                                                                                                 Score Pred.
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IBM PC Compatible
YSTEM: PC-DOS/MS-DOS
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INFORMATION
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1 No. 5756290th
           TELEPHONE: 1-312-744-0090
TELEPAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 6:
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ilarity 32.1%;
Conservative 9
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Amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy DE
COMPUTER: IBM PC COMPE
OPERATING SYSTEM: PC-1
                                                              CHARACTERISTICS
                                                                                                                                                  Peptide
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
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: Cyanobacterial and Plant A
: Carboxylase
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S KILIANRGEIALRILRTCEELGIGTI----AVHSTV-
                                                                                                                                                                                                                                                                                                                                                         Score 679.5; DB Pred. No. 1.2e-53
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                              NAME: Thomas E. No. 5756290thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SOFTWARE: CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01/956,700
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                                                                                                                                                                                                                                                                                                                                                      23.4%;
                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                     : 453 amino acids
Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Robert I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                  Linear
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                      168;
SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 679.5; DB 1;
Pred. No. 1.2e-53;
; Mismatches 166;
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                                                  Clark Street
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5792627thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,607
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                   : Floppy Disk,
IBM PC Compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    : 1-312-744-0090
1-312-755-4489
OR SEQ ID NO: 6:
                                Arnold, White 6
1 No. 5792627th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.4%;
ilarity 32.1%;
Conservative 9'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERISTICS
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: Arnold, 1
                                                                                                                                                                                                          ASCII-DOS
                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linear
                                             : 321 No.
Chicago
Illinois
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Best Local Similarity
Matches 168; Conser
                                                                                                                                      COMPUTER READABLE MEDIUM TYPE: F1
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; MOLECULE TYPE:
US-08-485-607-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR
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208

159

268

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Search completed: February 4, 2006, 18:14:38 Job time : 55 secs

5.1.7 Biocceleration Ltd version - 2006 GenCore (c) 1993 Copyright

model 3 using - protein search, OM protein ; Search time 248 Seconds (without alignments) 1590.284 Million cell updates/sec 2006, 18:05:17 4, February Run on:

US-10-633-835-2 2907 1 PPPDHKAVSQFIGGNPLETA.....LDGLIQDRLTAERPPADLAV

Title: Perfect score: Sequence:

559

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

residues 2166443 seqs, 705528306 Searched:

2166443 Total number of hits satisfying chosen parameters

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

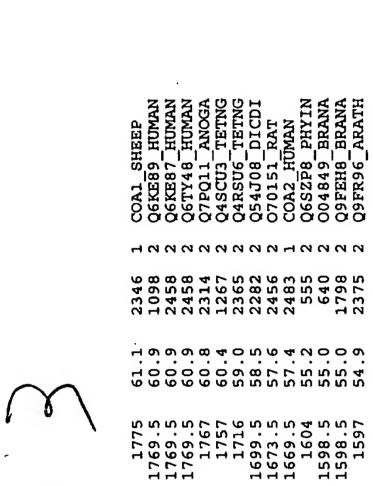
Database

UniProt_05.80:* 1: uniprot_sprot:* 2: uniprot_trembl:*

ve a printed, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.

STIMMARTES

SUMMARIES ID Description		2721 USTMA Q12721 ustilago	. Q5kfc9 crypto	Q55qt6 cryptoco	O60033 emericel	Q5b004 aspergil	Q4x1v2	Q7sbl5 neurospor	Q51yc2	Q4i878	Q6c134	Q6fkkB	P78820 schizosa	Q6cc91 yarrowia	O Q75ek8 ashbya g	Q5aam4	556000	_	P32874	042823 sacc)	Q6xda8 homo		P11497 rattu	Q6jiz0 mus muscu	Snm 6nm850		DROME Q9v346 dros	CHICK P11029 gall	7_DROME Q9v347 dros	IZ1_MOUSE	ייייים ו
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Length 1	18	2185	23	23	28	28	29	27	34	27	23	23	28	26	23	27	23	29	27	27	34	34	34	44	34	34	32	32	2482	34	5
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ovis aries homo sapien homo sapien anopheles g tetraodon n tetraodon n dictyosteli rattus norv homo sapien phytophthor brassica na brassica na arabidopsis

Q28559 Q6ke89 Q6ke87 Q6ty48 Q7pq11 Q4scu3 Q4rsu6 Q54j08 Q70151 Q68zp8 Q68zp8 Q9feh8

ALIGNMENTS

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                                                                        activity
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        is..;
1-201(1995).
1; -; Genomic_DNA.
                                                                      carboxylase
                                                                                             IEA.
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growth in Ustilago maydis.";

Mol. Gen. Genet. 249:191-201(1995).

EMBL; Z46886; CAA86983.1; -; Genomic-PIR; S60200; S60200.

HSSP; Q00955; 1004.

SMR; Q12721; 11-545.

GO; GO:0003989; F:acetyl-CoA carboxyl GO; GO:0009374; F:higase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR011761; ATP_GRASP.

InterPro; IPR0101882; Biotin_BS.

InterPro; IPR00089; Biotin_lipoyl.

InterPro; IPR00089; Biotin_lipoyl.

InterPro; IPR011763; COA_CT_C.

InterPro; IPR011763; Biotin_InterPro; IPR011763; I.

PROSITE; PS00775; ATP_GRASP; I.

PROSITE; PS00775; BIOTIN; UNKNOWN I.
                                                                                                                                                                                                                                                                                                                                       BIOTINYL LIPOYL;
COA CT CTER; 1.
COA CT NTER; 1.
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Conservative (
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PS50989;
PS50980;
PS50980;
PS00866;
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557; Conser
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Pfam; PF0105...
Pfam; PF02786;
-fam; PF02786;
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Best Local S
Matches 557
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SEQUENCE
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STRAIN=IMI103761;
MEDLINE=96086936; PubMed=7500941; DOI=10.1007/BF00290366,
Bailey A.M., Keon J.P.R., Owen J., Hargreaves J.A.;
"The ACC1 gene, encoding acetyl-CoA carboxylase, is esser
                                                                                                        Length
                                                                                                                              Indels
   "The genome sequence of Ustilago maydis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry
                                                                                   CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
6.4.1.2).
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Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae
NCBI_TaxID=5270;
                                                                                   8C2ECBF613483DF7
                                                                                                     Score 2907; DB 2;
Pred. No. 2.9e-189
0; Mismatches 0;
                                                            Genomic_DNA
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                                                preliminary data.

EMBL; AACP01000168; EAK85486.1;

Hypothetical protein.

SEQUENCE 2185 AA; 240063 MW;
                                                                          240063 MW;
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012721_USTMA PRELIMINARY;
012721;
01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-MAR-2004 (TrEMBLrel. 26, L
Acetyl CoA carboxylase (EC 6.
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O550T6;
O550T6;
13-SEP-2005 (TrEMBLrel. 31
13-SEP-2005 (TrEMBLrel. 31
13-SEP-2005 (TrEMBLrel. 31
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Complete
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STRAIN=JEC21;

PubMed=15653466; DOI=10.1126/science.1103773;

PubMed=15653466; DOI=10.1126/science.1103773;

PubMed=15653466; DOI=10.1126/science.1103773;

A Loftus E., Roncaglia P., Rowley D., Amedeo P., Bruno D., Vamathewan J., Funge E., Roncaglia P., Rowley D., Anlen J.E., Boodet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J., Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J., Markon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A., Mitchell T.G., Pertea M., Krogh H.L., Kroykinski M.I., Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A., Mitchell T.G., Pertea M., Shumway M., Specht C.A., Mitchell T.G., Pertea M., Wigher M.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., M., Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., M., Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., M., Myer N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., Science 307:1321-1324 (2005).

Expercoccus necformans...;

REMBL, AE017346; AAW44009:1; -; Genomic_DNA.

Science 307:1321-1324 (2005).

Expercol 1PR011761; ATPLEASP.

R. InterPro; IPR011761; ATPLEASP.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Acetyl-CoA carboxylase, putative.
ORFNames=CNF02180;
Cryptococcus neoformans var. neoformans JEC21.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomy
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=214684;
  DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESN
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Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback
Van Aken S., Fraser C.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR005481; CPaBe_L N.
InterPro; IPR005479; CPaBe_L N.
Pfam; PF02785; Biotin_carb_C; I.
Pfam; PF01039; Carboxyl trans; 1.
Pfam; PF01039; Carboxyl trans; 1.
Pfam; PF02786; CPSase_L_Chain; 1.
PROSITE; PS50975; ATP_GRASP; 1.
PROSITE; PS50975; ATP_GRASP; 1.
PROSITE; PS50979; BC; 1.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=CNBF2520;
Cryptococcus neoformans var. neoformans B-3501A.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycoramellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=283643;
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"Cryptococcus neoformans serotype D sequencing.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                           CRC64
                                                       DB 2; 1
1.2e-145; 74;
                                          5BD89138E
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                                                                                           d. No. 1.20
Mismatches
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No. 1
                                          E5BFB52
1.
UNKNOWN 1
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HKAVSOFIGGNPLETAPASPVADFIRKOGGHSVITKVLICNNGIAAVKEIRSIRKWAYET
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                                                                                                                                                                                                                                                                                                                                                                                              gene
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STRAIN=FGSC A26;

MEDLINE=99087906; PubMed=9871120; DOI=10.1007/8002940050410;

I solution and characterisation of the acetyl-CoA carboxylase genn from Aspergillus nidulans.;

Lurr. Genet. 34:379-385(1998).

EMBL; Y15996; CAA75926.1; -; Genomic_DNA.

R DISP; T30568; T30568.

R DISP; T30568; T30568.

R DISP; T30568; T30568.

R GO; GO:0009389; F:acetyl-CoA carboxylase activity; IEA.

GO; GO:0009524; F:biotin binding; IEA.

GO; GO:0008152; P:metabolism; IEA.

R InterPro; IPR001882; Biotin_carb_C.

R InterPro; IPR001764; BC.

R InterPro; IPR001763; COA_CT_N.

R InterPro; IPR001763; COA_CT_N.

R InterPro; IPR005481; CPase=\( \text{L} \) N.

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycete
Eurotiales; Trichocomaceae; Emericella.
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3.1e-140;
nes 87;
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COA_CT_CTER; 1.
COA_CT_NTER; 1.
CPSASE_1; UNKNOWN_1.
CPSASE_2; UNKNOWN_1.
                                                                                                                                                Created)
                                                                                                                                                                             . 26, Last (EC 6.4.1.
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Pfam; PF00364; Biotin lipoyl; 1.
Pfam; PF01039; Carboxyl trans; 1
Pfam; PF00289; CPSase L chain; 1
Pfam; PF02786; CPSase L chain; 1
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS50979; BC; 1.
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Best Local Similarity 74.8
Matches 415; Conservative
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PS50980;
PS00866;
PS00867;
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060033 EMENI
060033;
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L.2e-145;
         Genomic DNA
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EMBL; AAEY01000031; EAL20176.1; -; Genomi SMR; Q55QT6; 24-557.

G0; G0:0005524; F:ATP binding; IEA.

G0; G0:0009374; F:biorin binding; IEA.

G0; G0:0016874; F:ligase activity; IEA.

G0; G0:0008152; P:metabolism; IEA.

InterPro; IPR011761; ATP GRASP.

InterPro; IPR011764; BC.

InterPro; IPR011764; BC.

InterPro; IPR01089; Biotin BS.

InterPro; IPR01089; Biotin Carb.C.

InterPro; IPR010763; COA.CT.C.

InterPro; IPR011763; COA.CT.C.

InterPro; IPR011763; COA.CT.C.

InterPro; IPR011763; COA.CT.N.

InterPro; IPR011763; COA.CT.N.

InterPro; IPR011763; COA.CT.N.

InterPro; IPR005479; CPSase L.Chain; I.

Pfam; PF01039; Carboxyl trans; I.

Pfam; PF02786; CPSase L.Chain; I.

PROSITE; PS50975; ATP_GRASP; I.

PROSITE; PS50979; BC; I.

PROSITE; PS50989; COA.CT.CTER; I.

PROSITE; PS50980; COA.CT.CTER; I.

PROSITE; PS50980; COA.CT.CTER; I.

PROSITE; PS50980; COA.CT.NTER; I.

PROSITE; PS50986; CPSASE_I; UNKNOWN I.
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2237 AA;
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TGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=FGSC A4;

Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,

Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,

Buckpaller B., Butler J., Calvo S.E., Camarata J., Chang J.,

Choepel Y., Collymore A., Cook A., Cooke D., Corum B., DeArellano K.,

Diaz J.S., Dodge S., Ferreira P., FitzGerald M., Gage D., Galagan J.

Erickson J., Faro S., Graham L., Grand-Pierre N., Hafez N.,

A gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,

Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,

A rells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,

Mihova T., Mabbit R., McCarthy M., Meldrim J., Nguyen C., Nicol R.,

Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

A Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

Nielsen C.B., Norbu C., Schupback R., Seaman S., Severy P., Smirnov S.,

Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,

Roman J., Schauer B., Stange-Thomann N., Stojanovic N., Stubbs M.,

Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,

Nasiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,

Nau X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
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Smirnov S
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                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=227321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome Sequence of Aspergillus nidulans.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AACD01000104; EAA58101.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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05B004 EMENI PRELIMINARY;
05B004;
10-MAY-2005 (TrEMBLrel. 30, Las
10-MAY-2005 (TrEMBLrel. 30, Las
10-MAY-2005 (TrEMBLrel. 30, Las
Hypothetical protein.
ORFNames=AN6126.2;
Aspergillus nidulans FGSC A4.
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NGEEFKOLYNAVLGEVPGSPVFVMKLAGOARHLEVOLLADOYGNAISI FGRDCSVORRHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYET
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                                                                                                                                                                                                                                        Length 2288
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                         927E2518811EB1AB CRC64;
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 74.8%; Pred. No. 3.1e-140
Matches 415; Conservative 53; Mismatches 87
IEA.
TEA.
                                                                                                                                                                                                                         255182 MW;
                                                                                                                                                                                                                  1 protein.
2288 AA;
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SEQUENCE 22
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STRAIN=OR74A;
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HSSP;
SMR; C
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PCIPWSG
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KGIRKVE
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Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.

Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,

Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,

Rosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,

Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,

Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,

Keller N., Khouri H., Kotamoto K., Kobayashi T., Kulkarni R.,

Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,

A Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,

A Majoros W.H., May G.S., Muller B.L., Mohamoud Y., Molina M., Monod I Majoros W.H., Pertea M., Price C., Pritchard B.L., Quail M.A.,

Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,

Rabbinowitsch E., Sanders G., Sanchez M.,

Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,

Rakeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,

Machida M., Hall N., Barrell B., Denning D.W.;

"Genomic sequence of the pathogenic and allergenic filamentous fung Rapergillus fumigatus.";
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

Acetyl-CoA carboxylase.

Acetyl-CoA carboxylase.

ORFNames=Afu2g08670;

Aspergillus fumigatus Af293.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus

NCBI_TaxID=330879;
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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254941 MW; 21624CBC5FBA7ED8 CRC64;
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ed. No. 5.9e-140;
Mismatches 85;
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Pred.
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   573
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   559 SNKLTAERPDTTIAV
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Best Local Similarity
Matches 412; Conser
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STRAIN=A£293;
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                                                                  RESULT
Q4X1V2
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KIIEEAPVTIAKPATFQAMERAAVSLGKLVGYVSAGTVEYLYSHADDKFYFLELNPRLQV
                                                EHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTOR
                                                                           KPQPQCHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQF
                                                                                                                                                                                 GHIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLI
                                                                                                                                                                                                                                                                                             Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived
EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.
; AABX01000166; EAA33781.1; -; Genomic_DNA
; P24182; 1DV1.
Q7SBL5; 14-558.
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Biotin_carb_C.
Biotin_lipoyl.
Carboxyl_trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR011761; ATP_GRASP InterPro; IPR011764; BC.
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26,
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01-MAR-2004 (TrEMBLrel. 2
Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                       ODRLTAERPPADLAV
                                                                                                                                                                                                                                                                                                                                                                                                                      SNKLTAERPDPIVAV
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IPR000089;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

NCBI_TaxID=242507;
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n; PF01039; Carboxyl_trans; 1.

n; PF00289; CPSase_L_chain; 1.

site; PS50975; ATP_GRASP; 1.

site; PS50979; BC; 1.

site; PS50968; BIOTIN; 1.

site; PS50989; COA_CT_CTER; 1.

site; PS50980; COA_CT_NTER; 1.
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13-SEP-2005 (TrEMBLrel. 31
13-SEP-2005 (TrEMBLrel. 31
Hypothetical protein.
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NCLEOTIDE SEQUENCE.

AN ENTERLY O'LES,

BITTER B. Nusbeau C., Abebe A., Abouelleil A., Adekoya E.,

A Harbruster J., Bachanteang P., Baldwin J., Barry A.,

A Bayul T., Blitchreven B., Bloom T., Blye J., Bachalawskiy L.,

A Bayul T., Blitchreven B., Brunache A., Butler J., Calixee N.,

Bayul T., Blitchreven B., Brunache A., Butler J., Calixee N.,

Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixee N.,

Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixee N.,

Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixee N.,

Brickson J., Parina A., Paro S., Dodge S., Docley K., Dorje P.,

Brickson J., Parina A., Faro S., Perreira P., Fischer H.,

Brickson J., Parina A., Faro S., Perreira P., Fischer H.,

Brickson J., Parina A., Faro S., Perreira P., Fischer H.,

Brickson J., Parina A., Houde N., Hughes L., Hulme W., Habby E., Illev I.,

A Brickson J., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,

A Gorie K., Morole K., Kamar M., Kamar A., Highins H.,

Homan T., Horn A., Houde N., Hughes L., Hulme W., Habby E., Illev I.,

A Mells C., Kieu A., Klaner P., Lowine S., Lewis D., Lewis T.,

A Mells C., Kieu A., Mabbitt R., Macudonald J., Machen C., Major J.,

Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,

A Menirov J., Mihalev A., Mihova T., Mikkelsen T., Menga V., Moru K.,

A Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Merse J., Rogov P.,

Norbu N., O'donnell P., Okoawo O., O'leary S., Comotosho B.,

A Moryen N., Mulrain L., Munson S., Parin D., Parin M., Norses J., Milocal R., Mikcelsen C., Niszari M., Norbu C.,

Norbu N., O'donnell P., Okoawo O., O'leary S., Carropoules S., Rachupka T., Ramasamy U., Rameau R., Schupbach R., Seaman C., Settipali S., Radvinger S., Rather S., Theodore J., Troulmeang S., Tropham K.,

Boridmen M., Schupbach R., Seamen C., Settipali S., Maryopoul W.,

The Yenge S., Tsand T., Tsanes C., Wang S., Wangoul Y.,

The Wangel T., Whittaker C., Wilkinson J., Wu Se Y., Wangon S.,

Tamer A., Zody M., Lander E.,

Mangdi T., Whittaker C., Wilkinson J., Wu W
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Zhu H., Blackmon B.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
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                                                                                SEEGFEELYKAAASEIPGSPIFIMKLAGNARHLEVQLLADQYGNNISLFGRDCSVQRRHQ
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                                              GIRKAV
                                                                      NGEEFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQ
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                                   ; Sordariomycetes; Gibberella.
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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Eukaryota; Pungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Hypocreales; Nectriaceae; (NCBI_TaxID=229533;
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Venkataraman V.S., Viel n
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ORFNames=FG06580.1;
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STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
PubMed=15229592; DOI=10.1038/nature02579;
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomy
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=28985;
                                                                     Length
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el. 28, Last annotation update)
Saccharomyces cerevisiae YNR01
                                          EC40D82850B76583
                                                                   148; DB 2;
5. 2.3e-137;
atches 90;
              Genomic_DNA
                                                                   Score 2148; D)
Pred. No. 2.3e
4; Mismatches
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preliminary data.
EMBL; AACM01000259; EAA78365.1;
Hypothetical protein.
SEQUENCE 2271 AA; 254510 MW;
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OrderedLocusNames=KLLA0F06072g;
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06CL34;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
similar to sp|000955 Sacche
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IPR011762;
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IPR005481;
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IPR005482;
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Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Ratreat A., Memequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Nikolal R., Lemaiee M., Lesur I., Ma L., Muller H.,
Nicaud J.-M., Nikolal R., Lemaiee M., Lesur I., Ma L.,
Nicaud J.-M., Nikolak M., Ozier-Falogeropoulos O.,
A. Pellens S., Portier S., Richard G.-F., Streau M.-L., Suleau A.,
Swennen D., Tekais F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,
A. Wincker P., Soucier J.-L.,
Geniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,
Muncker P., Soucier J.-L.,
Telenome evolution in yeasts.",
I. Nature 430:35-44(2001)
I. Nature 430:35-44(2001)
I. Nature 430:35-44(2001)
I. Nature 430:35-44(2001)
I. Nature 430:35-44(2001)
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                       KPOPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSOF
EHPTTEMVTGVNLPSAQLQIAMGIPMHRIRDIRLLYGVDPKSASEIDFNFSTPESAKTQR
                                     GHIFAYGADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLI
                                                                                        Saccharomycetes; Candida.
                                                                                                                                                                                                                                                                                         sequence
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome L complete
OrderedLocusNames=CAGLOL10780g;
Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; mitosporic Saccharomycetales; Cand
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Biotin_carb_C.
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Carboxyl_trans.
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BIOTIN; 1.
BIOTINYL_LIPOYL;
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CPase D2 A
CPSase D2 A
In carb C; 1.
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Pfam; PF00364; Biotin_lipoyl; 1
Pfam; PF01039; Carboxyl_trans;
Pfam; PF00289; CPSase_L_chain;
Pfam; PF02786; CPSase_L_D2; 1.
PROSITE; PS50975; ATP_GRASP; 1.
PROSITE; PS50979; BC; 1.
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STRAIN=972 / HM123;
Saito A., Kazuta Y., Toh H., Kondo H., Tanabe T.;
Saito A., kazuta Y., Toh H., Kondo H., Tanabe T.;
"Biotin-dependent enzymes in Schizosaccharomyces pombe: cloning
"Biotin-dependent enzymes in Schizosaccharomyces pombe: noning
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P78820; 094557; Q09447; Q09576; Q09616; Q09667;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) (Cell untime)
6) [Includes: Biotin carboxylase (EC 6.3.4.14)].
Name=cut6; ORFNames=SPAC56E4.04c;
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomyces.
NCBI_TaxID=4896;
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                                       8B381EA1F3C99FC3
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Pred. No. 1.9e
73; Mismatches
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1 Similarity 70.7%;
391; Conservative
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=CLIB 122 / E 150;

PubMed=15229592; DOI=10.1038/nature02579;

PubMed=15229592; DOI=10.1038/nature02579;

A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Boisrame A., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

A Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                        NNERAIKFTVMATPDDLKVNADYIRMADQYVEVPGGSNNNNYANVELIVDIAERMNVHAV
                                         WAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGT
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|Q00955 Saccharomyces cerevisiae Acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=YALIOC11407g;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Dipodascaceae; Yarrowia.
NCBI_TaxID=4952;
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Wincker P., Souciet J.-L.,
"Genome evolution in yeasts.";
Nature 430:35-44(2004).
EMBL; CR382129; CAG82031.1; -; GARR: O6CC91; 33-574.
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| enzyme; Nucleotide-bi
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ATP-grasp.
Biotinyl/lipoyl.
Carboxyltransferase.
ATP (By similarity).
By similarity.
Biotin (covalent) (By similarity).
Coenzyme A (By similarity).
Coenzyme A (By similarity).
Coenzyme A (By similarity).
LYAIKATISLPRLFYRRLRTMAPRVASHF ---
LISQLSISSFFFILYFINHI (in Ref. 3).
E -> L (in Ref. 1).
A -> S (in Ref. 1).
A -> S (in Ref. 1).
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A -> S (in Ref. 1).
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Pred. No. 2e-133;
; Mismatches
GO, GO: 0000280; P:nuclear division; IMP.

InterPro; IPR011761; ATP_GRASP.

InterPro; IPR01182; Biotin_carb_C.

InterPro; IPR001882; Biotin_carb_C.

InterPro; IPR000029; Carboxyl_trans.

InterPro; IPR001763; COA_CT_C.

InterPro; IPR001763; COA_CT_C.

InterPro; IPR001763; COA_CT_C.

InterPro; IPR001763; COA_CT_C.

InterPro; IPR005481; CPASSE_D2_ATP_bd.

Pfam; PF00189; Carboxyl_trans; 1.

Pfam; PF00189; Carboxyl_trans; 1.

Pfam; PF00189; Carboxyl_trans; 1.

PROSITE; PS50968; Biotin_lipoyl; 1.

PROSITE; PS50989; COA_CT_CTER; 1.

PROSITE; PS50989; COA_CT_NER; 1.

PROSITE; PS50989; COA_CT_NER; 1.

PROSITE; PS50989; COA_CT_CTER; 1.

PROSITE; PS50989; COA_CT_NER; 1.

PROSITE; PS50989; COA_CT_NER; 1.

PROSITE; PS50989; COA_CT_CTER; 1.

PROSITE; PS50989; COA_CT_NER; 1.

PROSITE; PS50989; PS5098; 1.

PROSITE; PS50989; PS50989; PS50
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                                                            Name=AAR071W;
                               05-JUL-2004
05-JUL-2004
05-JUL-2004
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Pred. No. 5.4e
63; Mismatches
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011764; BC.
InterPro; IPR011764; BC.
InterPro; IPR001882; Biotin BS.
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Pfam; PF02785; Biotin carb C; I.
Pfam; PF00364; Biotin lipoyl; 1.
Pfam; PF00389; Carboxyl trans; 1.
Pfam; PF00188; Biotin lipoyl; 1.
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS50989; COA CT CTER; 1.
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PROSITE; PS50986; CPSASE 1; UNKNOWN 1.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Eremothecium NCBI_TaxID=33169;
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STRAIN=ATCC 10895;
PubMed=15001715; DOI=10.1126/science.1095781;
Dietrich F.S., Voegeli S., Brachat S., Lerch A.,
Mohr C., Poehlmann R., Luedi P., Choi S., Wing R
Gaffney T.D., Philippsen P.;
"The Ashbya gossypii genome as a tool for mappin
Saccharomyces cerevisiae genome.";
Science 304:304-307(2004).
EMBL; AE016814; AAS50436.1; -; Genomic_DNA.
SMR; Q75EK8; 16-566, 1480-2216.
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PubMed=15123810; DOI=10.1073/pnas.0401648101;
Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S., Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee Davis R.W., Scherer S.;
"The diploid genome sequence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
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); GO:0005524; F:ATP binding; IEA.

); GO:0009374; F:biotin binding; IEA.

); GO:0016874; F:ligase activity; IEA.

); GO:0008152; P:metabolism; IEA.

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Q00955;

Q1-APR-1993 (Rel. 25, Created)

Q1-OCT-1996 (Rel. 34, Last sequence update)

13-SEP-2005 (Rel. 48, Last annotation update)

Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: carboxylase (EC 6.3.4.14)].

Name=FAS3; Synonyms=ACC1; OrderedLocusNames=YNR016C; Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                              D57D403C36D7A290
                                                                                                                                                                                                                                                                                                                                ore 2061.5; DB 2;
ed. No. 1.9e-131;
Mismatches 98;
InterPro; IPR005479; CPSase D2 ATP bd.
Pfam; PF02785; Biotin carb C; I.
Pfam; PF00364; Biotin lipoyl; 1.
Pfam; PF01039; Carboxyl trans; 1.
Pfam; PF02786; CPSase L chain; 1.
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS50979; BC; 1.
PROSITE; PS50989; COA CT CTER; 1.
PROSITE; PS50980; COA CT CTER; 1.
PROSITE; PS509865; CPSASE 1; 1.
PROSITE; PS00866; CPSASE 2; UNKNOWN 1.
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                                                                                                                                                                                                                                            MUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

MEDLINE=97313269; PubMed=9169873;

Philippsen P., Kleine K., Poehlmann R., Duesterhoeft A., Hamberg K., Hegemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K., Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,

Altmann R., Angelo M., Dal Pero F., De Antoni A., del Rey F.,

Crouzet M., D'Angelo M., Dubois E., Fiedler T.A., Fleig U., Floeth M.,

Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N.,

Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N.,

A Gueldener U., Herbert C.J., Heumann K., Heuse Neitzel D.,

Hilbert H., Hinni K., Iraqui Houssaini I., Jacquet M., Jümenez A.,

Jonniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A.,

Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C.,

Messenguy F., Mewes H.-W., Moestl D., Nasr F., Nicaud J.-M.,

Miedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J.,

Rohl T.M., Purnelle B., Rebischung C., Remacha M.A., Revuelta J.L.,

Rohl T.M., Vubanus J.H.M., Valle G., Van Dyck L., Verhasselt P.,

Vierendeels F., Vissers S., Voet M., Volckaert G., Wach A.,

Wambutt R., Wedler H., Zollner A., Hani J.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV

and its evolutionary implications.";
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MEDLINE=21864552; PubMed=11875433; DOI=10.1038/nbt0302-301;

Ficarro S.B., McCleland M.L., Stukenberg P.T., Burke D.J., Ross M.M., Shabanowitz J., Hunt D.F., White F.M.;

"Phosphoproteome analysis by mass spectrometry and its application to Saccharomyces cerevisiae.";

Nat. Biotechnol. 20:301-305(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxyltransferas
                                                                                       NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 2015-2022.
MEDLINE=92262474; PubMed=1350093;
Al-Feel W., Chirala S.S., Wakil S.J.;
"Cloning of the yeast FAS3 gene and primary structure of yeast
         Saccharomycete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acetyl
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SUBCELLULAR LOCATION: Cytoplasmic.

SIMILARITY: Contains 1 ATP-grasp domain.

SIMILARITY: Contains 1 biotin carboxylation domain SIMILARITY: Contains 1 biotinyl-binding domain.

SIMILARITY: Contains 1 carboxyltransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced the between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no use as long as its content is in no way modified and removed.
 Saccharomycotina; Saccl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12663926; DOI=10.1126/science.1081366; Zhang H., Yang Z., Shen Y., Tong L.; "Crystal structure of the carboxyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
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TION: This protein carries three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carrier protein, biotin carboxylase, CATALYTIG ACTIVITY: ATP + acetyl-CoA
  Eukaryota; Fungi; Ascomycota; Saccharom
Saccharomycetales; Saccharomycetaceae;
NCBI_TaxID=4932;
                                                                                                                                                                                                         Sci. U.S.A.
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CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                        Acad.
                                                                                                                                                                                  carboxylase:. Natl. Acad
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Science 299:206
-!- FUNCTION: 1
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Ensembl; YNR016C; Saccharomyces cerevisiae.

R GO; S00005299; ACC1.

R GO; GO:0005789; C:endoplasmic reticulum membrane; IDA.

R GO; GO:0005739; C:mitochondrion; IDA.

R GO; GO:0005739; C:mitochondrion; IDA.

R GO; GO:0004075; F:biotin carboxylase activity; IMP.

R GO; GO:0006998; P:nuclear membrane organization and biogenesis; TAS

R GO; GO:000606; P:protein-nucleus import; IMP.

R InterPro; IPR011761; ATP_GRASP.

R InterPro; IPR011862; Biotin_BS.

R InterPro; IPR001882; Biotin_Carb_C.

InterPro; IPR00089; Biotin_lipoyl.

R InterPro; IPR000082; Carboxyl_trans.
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L->I: Raises Km for malonyl-CoA
factor of 20.
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Y->F: No effect.
R->S: Raises Km for malonyl-CoA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding, Biotin, Complete proteome,
n sequencing, Fatty acid biosynthesis, Ligase,
is, Multifunctional enzyme; Nucleotide-binding
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ATP-grasp.
Biotinyl/lipoyl.
Carboxyltransferase.
ATP (By similarity).
By similarity.
Biotin (covalent) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity
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(in Ref.
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E->0: Lowers ac
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InterPro; IPR011762; COA_CT_N.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005479; CPSase_D2_ATP_Dc
Pfam; PF02785; Biotin_lipoyl; 1.
Pfam; PF01039; Carboxyl trans; 1.
Pfam; PF02786; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_chain; 1.
PROSITE; PS50975; ATP_GRASP; 1.
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                                      ; A/B=1429-2233.
; A/B/C=1429-2233.
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; A/B/C=1482-2218.
; A/B/C=1482-2218.
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[-ray; A/B/C=1476-2233.

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COA_CT_NTER;
CPSASE_1; 1.
CPSASE_2; 1.
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BIOTIN, 1
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IPR011763;
IPR011762;
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1UYV; X-ray;
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1W93; X-ray;
1W96; X-ray;
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ct; Q00955; -.
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DOMAIN 58
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DOMAIN 701
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NP BIND 256
ACT SITE 383
BINDING 1731
BINDING 2034
BINDING 2034
BINDING 2035
MOD RES 1157
MUTÄGEN 1705
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PROSITE; PS50979;
PROSITE; PS00188;
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STRAIN=ATCC 36239 / CBS 767;

PubMed=15229592; DOI=10.1038/nature02579;

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Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L.; Muller H.,
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                                                                                                          PDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIR
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CA5816|CaACC1 Candida albicans CaACC1 acetyl-coenzyr carboxylase.
OrderedLocusNames=DEHA0B05632g;
Debaryomyces hansenii (Yeast) (Torulaspora hansenii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetels Saccharomycetales; Saccharomycetaceae; Debaryomyces.
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                                       Length
     CRC64
    0A335AAD9B1F8308
                                  Score 2060; DB 1;
Pred. No. 2.3e-131;
6; Mismatches 89;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Bellenz S., Porier S., Richard G.-F., Straub M.-L., Suleau A., Swennen D., Tekaia P., Weschowski-Louvel M. Westhofe E., Witth B., Zeniou-Mayer M., Zivanovic Y., Seniour-Mayer M., Zivanovic Y., Seniour-Mayer M., Zivanovic Y., Seniour-Mayer M., Thierry A., Bucuchier C., Canddron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.-L., Seniour-Mayer M., Thierry A., Mincker P., Souciet J.-L., Genomic DNA.

Rabuther 40.135-44/2004)

Rature 40.135-44/2004)

Rature 40.135-44/2004)

Rature 40.135-44/2004)

Rature 40.136-44/2004)

Rature 40.106894; Filter binding; IEA.

GO; GO:0009374; Filter B.

Rature 40.108093; Filter B.

Rature 40.108093; Filter B.

Rature 40.108093; Filter B.

Rature 40.108093; Botin Garb C.

Rature 40.108093; Botin Larans.

Rature 40.10809; Botin Lipoyl.

Rature 40.10809; Botin Lipoyl.

Rature 40.10809; Botin Lipoyl.

Rature 40.10809; Botin Lipoyl.

Rature 40.10809; Coacar M.

Rature 40.10809; Botin Lipoyl.

Rature 40.10809; Coacar M.

Rature 40.10809; Botin Lipoyl.

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Pred. No. 6.1e-130;
72; Mismatches 97;
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Seq. 4:69-70(1993).

Seq. 4:69-70(1993).

Seq. 4:69-70(1993).

COFACTOR: Biotin (By similarity).

SIMILARITY: Contains 1 ATP-grasp domain.

SIMILARITY: Contains 1 biotin carboxylation domain.

SIMILARITY: Contains 1 biotinyl-binding domain.

SIMILARITY: Contains 1 biotinyl-binding domain.

SIMILARITY: Contains 1 carboxyltransferase domain.

SIMILARITY: Contains 1 carboxyltransferase domain.

CAUTION: The reading frame from which this protein in translate has no Met initiation codon near to the 5'end. It does not seem be a pseudogene. There are no apparent frameshifts.
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n M.A.
                                                                                                                                                                                                                                                   YM832
                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=S288c / AB972;
MEDLINE=97313268; PubMed=9169872;
Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T. Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M. Rice P., Skelton J., Walsh S.V., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a conserveen the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictives as long as its content is in no way modified and this state
Saccharomycete
                                                                                                                                                                                                                                                   ORFNames=YM8261.01C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGD; S000004820; HFA1.
GO; GO:0005739; C:mitochondrion; IDA.
GO; GO:0003989; F:acetyl-CoA carboxylase activity; IGI.
GO; GO:0006633; P:fatty acid biosynthesis; IGI.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
InterPro; IPR001882; Biotin_BS.
                                                                                                                                                                                                                                    HFA1 protein.
Name=HFA1; OrderedLocusNames=YMR207C; ORFNames=YM8261
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaces.
NCB1_TaxID=4932;
                                                                                                                                                                                                                        update)
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EMBL; Z48755; CAA88647.1; -; Genomic_DNA.

EMBL; Z22558; CAA80280.1; -; Genomic_DNA.

PIR; S55089; S55089.

HSSP; Q00955; 10D4.

SMR; P32874; 90-634.

GermOnline; 142882; -.

Ensembl; YMR207C; Saccharomyces cerevisiae.

SGD; S000004820; HFA1.
                                                                                                                                                                                                             update)
                                                                                                                                                                                                (Rel. 27, Created)
(Rel. 34, Last sequence up
(Rel. 48, Last annotation
                                                                                                                                                                         PRT;
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MEDLINE=94146412; PubMed=7906156;
Kearsey S.E.;
"Identification of a Saccharomyce
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|629 SKKLTSERPDHIVAV
                                                                                     ODRLTAERPPADLAV
                                                                                                                                                                         STANDARD;
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Nature 387:90-93(1997)
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01-OCT-1996
13-SEP-2005
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PPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWA
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Biotinyl/lipoyl.

Carboxyltransferase.

ATP (By similarity).

By similarity.

Biotin (covalent) (By similar

F -> L (in Ref. 2).

WW, 08727A301549DA92 CRC64;
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Pred. No. 1.1e-119;
5; Mismatches 94;
InterPro; IPR005482; Biotin_lipoyl.
InterPro; IPR00022; Carboxyl_trans.
InterPro; IPR011762; Carboxyl_trans.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005481; CPase_LN.
InterPro; IPR005479; CPSase_LN.
InterPro; IPR005479; CPSase_LN.
InterPro; IPR005479; CPSase_LOD_C; I.
Pfam; PF00289; CPSase_LOD_N; I.
Pfam; PF00289; CPSase_LOD_N; I.
PROSITE; PS50975; ATP_GRASP; I.
PROSITE; PS50989; COA_CT_CTER; I.
PROSITE; PS50989; COA_CT_CTER; I.
PROSITE; PS50980; COA_CT_CTER; I.
PROSITE; PS50990; CO
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Best Local Similarity 64.3%;
Matches 355; Conservative
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 IRKCTNGEEFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSV
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A Sinilnikova O.M., Ginolhac S.M., Magnard C., Leone M., Ancz Moreau K., Thompson D., Coutanson C., Bonadona V., Lasset C Goldgar D.E., Joulin V., Dalla Venezia N., Lenoir G.M.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY237919; AAP69841.1; -; mRNA.

ENSG0000132142; Homo sapiens.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0008152; P:metabolism; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR011761; ATP GRASP.

InterPro; IPR011764; BC.

InterPro; IPR001882; Biotin BS.

InterPro; IPR001882; Biotin BS.

InterPro; IPR001763; COA CT C.

InterPro; IPR011763;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 27, Created)
. 27, Last sequence update)
. 27, Last annotation update
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BIOTINYL LIPOYL;
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Pfam; PF00364; Biotin lipoyl; 1.
Pfam; PF01039; Carboxyl trans; 1.
Pfam; PF00289; CPSase L chain; 1.
Pfam; PF02786; CPSase L D2; 1.
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS50979; BC; 1.
PROSITE; PS50968; BIOTINY, 1.
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05-JUL-2004 (TrEMBLrel. 27, I
05-JUL-2004 (TrEMBLrel. 27, I
Acetyl-CoA carboxylase alpha.
Name=ACACA;
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QEXDA8 HUMAN PRELIMINARY;
QEXDA8;
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DVAEQTD
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Acetyl-coenzyme A carboxylase like carboxylase (Fragment)
Name=ALC;
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
EMBL; D78165; BAA24410.1; -; Genomic_DNA.
HSSP; Q00955; 10D4.
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Pred. No. 1.1e-119;
6; Mismatches 94;
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CPSASE_2; UNKNOWN_1
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COA CT CTER; 1.
COA CT NTER; 1.
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259162 MW;
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ilarity 64.3%;
Conservative 80
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33 YEAST
042823 YEAST PRELIMINARY;
042823;
LDDLILKNLSSD
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PS50968;
PS50989;
PS50980;
PS00866;
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STRAIN=SP1;
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Primates; Catarrhini; Hominidae
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                                                    Indels
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MEDLINE=22709197; PubMed=12810950; DOI=10.1073/pnas
Mao J., Chirala S.S., Wakil S.J.;
"Human acetyl-CoA carboxylase 1 gene: presence of the terogeneity at the 5'-untranslated mRNA region.";
Proc. Natl. Acad. Sci. U.S.A. 100:7515-7520(2003).
                         F1F0A518F8824FFC
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Last sequence update)
Last annotation update
                                      Score 1791; DB 2;
.Pred. No. 6e-113;
79; Mismatches 103;
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Mammalia; Eutheria; Euarchontoglires;
PS50989; COA_CT_CTER; 1.
PS50980; COA_CT_NTER; 1.
PS00866; CPSASE_1; 1.
PS00867; CPSASE_2; UNKNOWN
2346 AA; 265554 MW; F1E
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                                      ch 61.6%; 1 Similarity 63.8%; 345; Conservative
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Q7Z561;
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2004 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
Acetyl-CoA carboxylase 1.
Name=ACC1;
Homo sapiens (Human).
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Matches 345
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ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIP
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AC156BCBD15F77AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY315627; AAP94122.1; -; mRNA. HSSP; P24182; 1DV1. Ensembl; ENSG0000132142; Homo sapiens GO; GO:0005524; F:ATP binding; IEA. GO; GO:0009374; F:biotin binding; IEA. GO; GO:0016874; F:ligase activity; IEA. GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                         InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
InterPro; IPR011764; BC.
InterPro; IPR0101882; Biotin_BS.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR00082; Carboxyl trans.
InterPro; IPR000022; Carboxyl trans.
InterPro; IPR011762; COA_CT_C.
InterPro; IPR011762; COA_CT_C.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR005481; CPase_D2_ATP_bd.
Pfam; PF02785; Biotin_carb_C; I.
Pfam; PF00289; Carboxyl trans; 1.
Pfam; PF00289; CPSase_L_chain; 1.
Pfam; PF00289; CPSase_L_chain; 1.
PROSITE; PS50975; ATP_GRASP; 1.
PROSITE; PS50989; COA_CT_CTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00866; CPSASE_1; 1.
PROSITE; PS00866; CPSASE_2; UNKNOWN 1.
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MEDLINE=89264558; PubMed=2566999;
Luo X.N., Park K., Lopez-Casillas F., Kim K.-H.;
"Structural features of the acetyl-CoA carboxylase gene: mechanisms for the generation of mRNAs with 5' end heterogeneity.";
Proc. Natl. Acad. Sci. U.S.A. 86:4042-4046(1989).
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from
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MEDLINE=88296498; PubMed=2900138;
Munday M.R., Campbell D.G., Carling D., Hardie D.G.;
"Identification by amino acid sequencing of three major regulation sites on rat acetyl-CoA carboxylase.";
Eur. J. Biochem. 175:331-338(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Wistar; TISSUE=Liver;
MEDLINE=94237850; PubMed=7910165;
Winz R., Hess D., Aebersold R., Brownsey R.W.;
"Unique structural features and differential phosphorylation of 280-kDa component (isozyme) of rat liver acetyl-CoA carboxylaseJ. Biol. Chem. 269:14438-14445(1994).
-!- FUNCTION: Catalyzes the rate-limiting reaction in the bioge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    without inhibitor
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MEDLINE=88320328; PubMed=2901088;
Lopez-Casillas F., Bai D.-H., Luo X., Kong I.-S., Hermodson M
                                                                                                                                                                                                                 [Includes:
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; S
Muroidea; Muridae; Murinae; Rattus.
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                                                                                                                      P11497; P97902;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha)
carboxylase (EC 6.3.4.14)}.
Name=Acaca; Synonyms=Acac;
Rattus norvegicus (Rat).
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Sci. U.S.A. 85:5784-5788(1988)
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MEDLINE=90337981; PubMed=1974251;
Kong I.-S., Lopez-Casillas F., Kim K.-H.;
"Acetyl-CoA carboxylase mRNA species with sequence for Ser-1200 phosphorylation.";
J. Biol. Chem. 265:13695-13701(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89289706; PubMed=2567668;
Bai D.-H., Moon T.-W., Lopez-Casillas F.,
"Analysis of the biotin-binding site on a
                                                                                                                2345
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Lopez-Casillas F., Kim K.-H.;
"Heterogeneity at the 5' end of remRNA. Lipogenic conditions enhanceliver.";
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               63
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this statement
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ATP-grasp.
1 817 Biotinyl/lipoyl.
7 2193 Carboxyltransferase.
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 three
             carboxylase,
                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse as long as its content is in no way modified and thi
                                                                                                                                                                                                                                                                     1 ATP-grasp domain.
1 biotin carboxylation domain.
1 biotinyl-binding domain.
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    biotin carboxyl carrier protein, b
carboxyltransferase.
- CATALYTIC ACTIVITY: ATP + acetyl-C
+ malonyl-CoA.
- CATALYTIC ACTIVITY: ATP + biotin-c
= ADP + phosphate + carboxybiotin-
COFACTOR: Biotin.
- COFACTOR: Biotin.
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3L; M26731; AAA40652.1; -; Genomic_L
3L; M26195; AAA40654.1; -; mRNA.
3L; M26196; AAA40655.1; -; mRNA.
3L; M26197; AAA40656.1; -; mRNA.
3L; M25315; -; NOT_ANNOTATED_CDS; mFR; A35578; A35578.
3F; Q00955; 10D4.
3embl; ENSRNOG0000034013; Rattus no
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Biotin_lipoyl.
Carboxyl_trans.
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COA CT CTER; 1.
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|; PF01039; Carboxyl trans; 1. |
|; PF00289; CPSase L chain; 1. |
|; PF02786; CPSase L D2; 1. |
|; PS50975; ATP GRASP; 1. |
||TE; PS50979; BC; 1. |
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D; GO:0004075;
D; GO:0016874;
D; GO:0008152;
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Glires; Rodentia; Sciurogn
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Coenzyme A (By similar Coenzyme A (By similar Coenzyme A (By similar Phosphoserine.
Phosphoserine.
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Missing (in isoform 2)
/FTId=VSP_011753.
                                                                    Score 1785; DB 1;
Pred. No. 1.5e-112
80; Mismatches 103
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Mammalia; Eutheria; Euarchontoglires; (
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN=C57BL/6J; TISSUE=Heart;
Mao J., Wakil S.J.;
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(TrEMBLrel. 27, 1)
(carboxylase 2.
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Matches 344; Conservative
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0B8649F5D2CF1C8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 63.8%; Score 1783.5; DB 2 Similarity 63.8%; Pred. No. 2.1e-112; 6; Conservative 73; Mismatches 108;
CT-2003) to the EMBL/GenBank/DDBJ d
94; AAS13686.1; -; mRNA.
13; C:biotin carboxylase complex; I
24; F:ATP binding; IEA.
75; F:biotin carboxylase activity;
74; F:ligase activity; IEA.
52; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50975; ATP_GRASP; 1.
PS50979; BC; 1.
PS50968; BIOTINYL_LIPOYL; 1.
PS50989; COA_CT_CTER; 1.
PS50980; COA_CT_NTER; 1.
PS00866; CPSASE_1; UNKNOWN_1.
PS00867; CPSASE_2; UNKNOWN_1.
PS00589; PTS_HPR_SER; UNKNOWN_1.
PS00589; PTS_HPR_SER; UNKNOWN_1.
                                                                                                                                               InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
InterPro; IPR0105482; Biotin_carb_C.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR011762; Carboxyl_trans.
InterPro; IPR011762; COA_CT_C.
InterPro; IPR011762; COA_CT_C.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR005481; CPase_L_N.
InterPro; IPR002114; HPr_SerP_S.
Pfam; PF02785; Biotin_lipoyl; 1.
Pfam; PF01039; Carboxyl_trans; 1.
Pfam; PF01039; Carboxyl_trans; 1.
Pfam; PF0289; CPSase_L_Chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
PROSITE; PS50975; ATP_GRASP; 1.
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LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD-
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ENZYME REGULATION: By phosphorylation (By similarity).
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Euarchontoglires; Primates; Catarrhini; H
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PubMed=15302935; DOI=10.1073/pnas.0404720101;

Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E.,

Li J., Cohn M.A., Cantley L.C., Gygi S.P.;

"Large-scale characterization of HeLa cell nuclear phospho

Proc. Natl. Acad. Sci. U.S.A. 101:12130-12135(2004).

-!- FUNCTION: Catalyzes the rate-limiting reaction in the

of long-chain fatty acids. This protein carries three

biotin carboxyl carrier protein, biotin carboxylase, a
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MEDLINE=95249602; PubMed=7732023;
Abu-Elheiga L., Jayakumar A., Baldini A., Chirala Abu-Elheiga L., Jayakumar A., Baldini A., Chirala "Human acetyl-CoA carboxylase: characterization, matuman acetyl-CoA carboxylase: characterization, mand evidence for two isoforms.";

Proc. Natl. Acad. Sci. U.S.A. 92:4011-4015(1995).
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01-NOV-1997 (Rel. 35, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha)
carboxylase (EC 6.3.4.14)].
Name=ACACA, Synonyms=ACAC, ACC1, ACCA;
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Mammalia; Eutheria;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
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MW; 6995C534B054FE02 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; ALS96447; CAI25271.1; -; Genomic_DNA.
EMBL; ALS96525; CAI24019.1; -; Genomic_DNA.
EMBL; ALS96252; CAI24019.1; -; Genomic_DNA.
EMBL; ALS96252; CAI25271.1; JOINED; Genomic_DNA.
EMBL; ALS96447; CAI24019.1; JOINED; Genomic_DNA.
GO; GO:0009343; C:Biotin carboxylase complex; IEA.
GO; GO:0009374; F:Biotin binding; IEA.
GO; GO:0009374; F:Biotin binding; IEA.
GO; GO:0004075; F:Biotin carboxylase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP GRASP.
InterPro; IPR011764; BC.
InterPro; IPR000892; Biotin_Carb C.
InterPro; IPR00082; Carboxyl_trans.
InterPro; IPR011763; COA_CT_C.
InterPro; IPR011764; COA_CT_C.
                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Pred. No. 2
                                                                                                                                                           01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequentialy-2005 (TrEMBLrel. 30, Last annot Acetyl-Coenzyme A carboxylase.
Name=Acac; ORFNames=RP23-123010.1-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000085, Carbox, InterPro; IPR011763; COA_CT_C. InterPro; IPR011762; COA_CT_C. InterPro; IPR011762; COA_CT_N. InterPro; IPR005481; CPase L N. InterPro; IPR005479; Cphp_Bynth_L_D2 Pfam; PF01039; Carboxyl_trans; 1. Pfam; PF01039; Carboxyl_trans; 1. Pfam; PF01039; CPSase_L_chain; 1. Pfam; PF02786; CPSase_L_chain; 1. Pfam; PF02786; CPSase_L_chain; 1. Pfam; PF02786; CPSase_L_D2; 1.
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larity 63.6%;
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Submitted (FEB-2005)
EMBL; AL596447; CAI25
EMBL; AL596252; CAI24
EMBL; AL596252; CAI25
EMBL; AL596447; CAI25
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(FEB-2005)
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Coenzyme A (By similarity).
Phosphoserine.
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
Phosphoserine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ty acid biosynthesis; Ligase; Lipid
Nucleotide-binding; Phosphorylation
                                                                                                                                                                                 s Swiss-Prot entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EMEuropean Bioinformatics Institute. There are no restras long as its content is in no way modified and this s
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A (By similarity).
A (By similarity).
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                               SUBCELLULAR LOCATION: Cytoplasmic.

TISSUE SPECIFICITY: Expressed in brain, placental, muscle, renal, pancreatic and adipose tissues; explevel in pulmonary tissue; not detected in the live SIMILARITY: Contains 1 ATP-grasp domain.
SIMILARITY: Contains 1 biotin carboxylation domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
  first
                                                                                                                                                                                                                                                                                                                                                                                       activity; TAS
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Biotinyl/lipoyl.
Carboxyltransferase.
ATP (Potential).
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   acid biosynthesis;
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Biotin (covalent)
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61; ATP_GRASP.
64; BC.
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138928; I38928.
; Q00955; 10D4.
mbl; ENSG0000132142; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               Biotin BS.
Biotin Carb C.
Biotin lipoyl.
Carboxyl trans.
COA CT C.
COA CT C.
COA CT N.
CPase L N.
CPSase D2 ATP b
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Ji PR011761; ATF

Lerpro; IPR011764; BC.

Lerpro; IPR011882; Bioti.
Interpro; IPR001882; Bioti.
Interpro; IPR000022; Carboxy
DR Interpro; IPR011763; COA CT N
DR Interpro; IPR011763; COA CT N
DR Interpro; IPR011763; COA CT N
DR Interpro; IPR011763; COA CT N
DR Interpro; IPR011763; COA CT N
DR Interpro; IPR011763; COA CT N
DR Interpro; IPR011763; COA CT N
DR Interpro; IPR0136481; CPSase D2
Rem; PF02785; Biotin Carb C; I
Pfam; PF01039; Carboxyl trans; 1
Pfam; PF01039; Carboxyl trans; 1
Pfam; PF02786; CPSase L Chain; 1
Pfam; PF02786; CPSase L D2; 1

ROSITE; PS50989; COA CT C

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COA CT NTER; 1.
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CPSASE 2; 1.
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ilarity 63.6%;
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A Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
A Fosler C., Gabriellan A.E., Garrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegwam C.,
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ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIP
                                                                                                                                                                                                                                                                                                                                          SENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFAGSQFGHCFSWGENREEAI
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9V346 DROME PRELIMINARY; PRT; 2323 AA. Q9V346; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 10-MAY-2005 (TrEMBLrel. 30, Last annotation update) CG11198-PB, isoform B (GH12002p).
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A Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S. Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S. Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A. Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;
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Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George
Hoskins R., Stapleton M., Pacléb J., Park S., Svirskas R., Smit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUCLEOTIDE SEQUENCE.
MEDLINE=22426070; PubMed=12537573;
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"The transposable elements of the Drosophila melanogaster a genomics perspective.";
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Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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Yu C., Rubin G
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mRNA.
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Pred. No. 3.4e
9; Mismatches
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                                    EMBL; ALLLSON-.
HSSP; Q00955; 10D4.
FlyBase; FBgn0033246; CG11198.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:biotin binding; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
InterPro; IPR001882; Biotin_BS.
InterPro; IPR00089; Biotin_lipoyl.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000022; Carboxyl_trans.
InterPro; IPR011763; COA_CT_C.
InterPro; IPR011763; COA_CT_C.
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CPSASE 2; UNKNOWN 1
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.IPR005481; COA CT N.
erPro; IPR005479; CPSase L N.
i; PF02785; Biotin carb C; 1.
i; PF001039; Carboxyl trans; 1.
i; PF00289; CPSase L chain; 1.
PF02786; CPSase L chain; 1.
TE; PS50975; ATP GRASP; 1.
TE; PS50979; BC; 1.
TE; PS50989; COA CT CTER; 1.
TE; PS50980; COA CT NTER; 1.
TE; PS50980; COA CT CTER; 1.
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         Submitted (JUN-2002) to the EMBL; AE003839; AAF59156.2; EMBL; AY119502; AAM50156.1;
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Local Similarity 64.2%;
Les 342; Conservative (
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; IPRO11763;
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PROSITE;
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Pfam; PF0
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Stt. 212:98-102(1987).

NCTION: Catalyzes the rate-limiting reaction in the biogenesis long-chain fatty acids. This protein carries three functions:
                                                                                                                      Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasianinae
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                                                                                                                                                                                                                                                                                    MEDLINE=87106011; PubMed=2879745; DOI=10.1016/0014-5793(87)8156
Takai T., Wada K., Tanabe T.;
"Primary structure of the biotin-binding site of chicken liver
                                                                                                                                                                                                                                                                                                                                                                                                                         protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation.
atty acid biosynthesis; first (rate-1
                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                       01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: Biotin carboxylase (EC 6.3.4.14)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is produced through
                                                                                                                                                                                                                       carboxylase
                                                                                                                                                                                                                                                                                                                                                                                        ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: Cytoplasmic.
Contains 1 ATP-grasp domain.
Contains 1 biotin carboxylation domain.
Contains 1 biotinyl-binding domain.
Contains 1 carboxyltraneform
                                                                                                                                                                                                                                                                                                                                                                                                             ATP + biotin-carboxyl-carrier practical carboxybiotin-carboxyl-carrier
                                                                                                                                                                                                                                                                                                                                                                                        + HCO(3)(-)
                                                                                                                                                                            PROTEIN SEQUENCE
                                                                                                                                                                         NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUEN
TISSUE=Liver;
MEDLINE=88139305; PubMed=2893793;
Takai T., Yokoyama C., Wada K., Tanabe T.;
"Primary structure of chicken liver acetyl-CoA
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                                                                                                                                                                                                                                                                                                                                                                                       acetyl-CoA
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CPase_L N.
CPSase_D2_ATP_bd.
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Biotin_carb_C.
Biotin_lipoyl.
Carboxyl_trans.
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                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -; mRNA.
                                                                                                                 Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
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TISSUE=Liver;
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n fatty
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                                                                                                                                                                                                                                                                                                                                                                biotin carboxyl carrier p
carboxyltransferase.
CATALYTIC ACTIVITY: ATP +
+ malonyl-CoA.
CATALYTIC ACTIVITY: ATP +
= ADP + phosphate + carbo
COFACTOR: Biotin.
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; Q00955; 1OD4.
mbl; ENSGALG0000005439
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EMBL; X05019; CAA28675.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC.
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Long-chain
                                                                                                          (Chicken)
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IPR011763;
IPR011762;
IPR005481;
IPR005479;
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IPR005482;
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                                                                                                                                                                                                                                from cDNA sequence
                                                                                                                                                                                                                                                                                                                         carboxylase."
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SIMILARITY:
SIMILARITY:
SIMILARITY:
                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                           gallus
                                                                                                                                                                                                                                                                                                                                 EBS Lett. 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY:
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                                                                                                 Name=ACAC
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HSSP;
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                                                                                                                                                                                                                                                           Direct protein sequencing;
is; Ligase; Lipid synthesis;
e; Nucleotide-binding; Phosphorylation.

Blotin carboxylation.

ATP-grasp.

Biotinyl/lipoyl.

Carboxyltransferase.

ATP (Potential).

By similarity.

By similarity.

Coenzyme A (By similarity).

Coenzyme A (By similarity).

Coenzyme A (By similarity).

Coenzyme A (By similarity).

Phosphoserine (By similarity).

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Pred. No. 3.4e-112;
; Mismatches 103;
Pfam; PF02785; Biotin_lipoyl; 1.

Pfam; PF00364; Biotin_lipoyl; 1.

Pfam; PF00289; Carboxyl_trans; 1.

Pfam; PF00289; CPSase_L_chain; 1.

PROSITE; PS50975; ATP_GRASP; 1.

PROSITE; PS50968; BIOTINYL LIPOYL; 1.

PROSITE; PS50989; COA_CT_CTER; 1.

PROSITE; PS50980; COA_CT_CTER; 1.

PROSITE; PS50980; COA_CT_CTER; 1.

PROSITE; PS50986; COA_CT_CTER; 1.

PROSITE; PS00866; CPSASE_1; 1.

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NUCLEOTIDE SEQUENCE.

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RAY MEDIANE-210-5006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adama M.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D., Antenderson S.N., Sutton G.G., Mortman J.E., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Mortman J.E., Yandell M.D., Zhang Q., Chen L.X., Rathorner M., Handerson S.N., Satton G.G., Mortman J.E., Manner E.G., Melson C.R., Miklos G.L.G., Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Wan K.H., Doyle C., Bazerle E.G., Nelson C.R., Miklos G.L.G., Abril J.F., Abbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Wan K.H., Doyle C., Berrer E.G., Helt G. Nelson C.R., Miklos G.L.G., Abril J.F., Abbayani A., Bernan B.P., Banddari D., Bolshakov S., Butler H., Cadieu E., Center A., Miklos G.L.G., Burtis S.C., Busam D.A., Butler H., Cadieu E., Center A., Dunbor B. Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Dunbor G., Dunbor G., Dunbor B., Delcher A., Deng Z., Mays A.D., Dew J., Dietz S.M., Dubbin K.J., Evangellstac C.C., Perrac C., Perrac B., Gorrell J.J.H., Gu Z., Guan P., Harris M., Harris M., Harris M., Allali M., Kalush F., Karpen G.H., Milshina N.U., March Y., Musskern D.R., Melson D.R., Match C., Scheeler F., Shan H., Nalson D.R., Melson D.R., March W., Sunger M., Perley M., Walson D.R., Melson M., Stupski M.P., Smith T., Shue B.C., Spradling A.C., Schalberon M., Stupski M.P., Wall S., March M., Walsenberd J.C., Wallen S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Walliams S.M., W
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                 CG11198-PA, isoform A.
CG11198-PA, isoform A.
Name=CG11198; Name=CG11198; Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Prhydroidea; Drosophilidae; Drosophila.
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on update)
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MEDLINE=22426070; PubMed=12537573;
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"The genome sequence of Dro
Science 287:2185-2195(2000)
Q9V347 DROME PRELIMINARY
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01-MAR-2004
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                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                               genome:
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                 "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                              Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic
                                                  a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
                                                                                                                                                                                                                                     Genome Biol. 3: RESEARCH0083.1-RESEARCH0083.22(2002)
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Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer
Hoskins R., Stapleton M., Pacleb J., Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPSASE 1; UNKNOWN 1
CPSASE 2; UNKNOWN 1; 278596 MW; F0E6
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FlyBase; FBgn0033246; CG11198.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:biotin binding; IEA.
GO; GO:0016874; F:ligase activity; IEG; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR01184; BC.
InterPro; IPR001882; Biotin_carb_C.
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Biotin lipoyl.
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Pfam; PF00364; Biotin lipoyl; 1.
Pfam; PF01039; Carboxyl trans; 1.
Pfam; PF02289; CPSase L chain; 1.
Pfam; PF02786; CPSase L D2; 1.
PROSITE; PS50975; ATP GRASP; 1.
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Q6JIZ1 MOUSE

ID Q6JIZ1 MOUSE PRELIMINARY; PRT; 2345 AA.

AC Q6JIZ1.

DT Q6JIZ1;

DT O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DT O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DT O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DT O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DT O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)

OF Acetyl-CoA carboxylase 1.

GN Name=Acaca; Synonyms=Acac;

OS Mus musculus (Mouse).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
                                                                 VMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKA
                                                                                           ELL--HK
            HKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQ
                    KPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEARKOMVISLK
                                                                                                                                                          QACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVF
                                                                                                                        ENPOTGF
                                                                                                                                      ENPDEGF
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EYIKMADHYVPVPGGSNNNNYANVELIVDIALRTQVQAVWAGWGHASENPKLP
                                                                                                                      GIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTORKPOPOGHVVACRITA
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                                                                                                                                                                                                                                                                                                                                                                    ARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                                                                                                                                                    TVSDDVYOQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKOLYNAVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                          AENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENPDEGFKPSSGTVQELNFRSNKNVWGYFSVAAAGGLHEFADSQFGHCFSWGENREEAI
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MEDLINE=21378179; PubMed=11485560; DOI=10.1042/0264-6021:3580127;
Mao J., Marcos S., Davis S.K., Burzlaff J., Seyfert H.-M.;
"Genomic distribution of three promoters of the bovine gene encoding acetyl-CoA carboxylase alpha and evidence that the nutritionally regulated promoter I contains a repressive element different from th
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Ruminantia
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                                                    CRC64;
                                                                               Length
                                                                                                         Indel
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Fecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                       WN 1.
D483B4CECCF6C7D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .pha)
                                                                            Score 1776; DB 2;
Pred. No. 6.4e-112;
; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COAL BOVIN STANDARD; PRT; 2346 AA. Q9TTS3; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 48, Last annotation update) Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-algrarboxylase (EC 6.3.4.14)].

Name=ACACA; Synonyms=ACAC, ACCA;
                               UNKONOWN
MW; D48
                                                                                                       19;
           CT_NTER;
; COA_C1_;

5; CPSASE_1; 1

7; CPSASE_2; U
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larity 63.4%;
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        PS50980;
PS00866;
PS00867;
2345 AA
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343; Conser
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141

197

--KETMMSDQGF

257

EGGGGKGIRKCTNGEEFKOLYNAVL

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457

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437

510

--HVPCPRGHVIAARI

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570

161

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LKVNADY I RMADOYVEVPGGSNNNNYANVDL I VDVAERAGVHAVWAGWGHASENPRLPES
     ASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
                    GEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPE
                                                                                                                                                                                                                                                                 AEVPGSPIFVMRLAKQSRHLEVQILADQYGNAISLFGRDCSVQRRHQKIIEEAPAAIATP
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Gene 154:271-275(1995)
-!- FUNCTION: Catalyze
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13-SEP-2005
Acetyl-CoA ca
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Q28559;
15-JUL-1998
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        Biochem. J. 358:127-135(2001).

Biochem. J. 358:127-135(2001).

-!- FUNCTION: Catalyzes the rate-limiting reaction in the biogenesis of long-chain fatty acids. This protein carries three functions: biotin carboxyl carrier protein, biotin carboxylase, and carboxyltransferase (By similarity).

-!- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate + malonyl-CoA.

-!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein.

-!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein.

-!- COFACTOR: Biotin.

-!- COFACTOR: Biotin.

-!- ENZYME REGULATION: By phosphorylation (By similarity).

-!- PATHWAY: Long-chain fatty acid biosynthesis; first (rate-limiting)
                                                                                         hosphate
                                                                                                                                                                                    imiting)
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Biotin (covalent) (By Similarity).
Coenzyme A (By Similarity).
Coenzyme A (By Similarity).
Coenzyme A (By Similarity).
Phosphoserine (By Similarity).
Phosphoserine (By Similarity).
Phosphoserine (By Similarity).
Phosphoserine (By Similarity).
Phosphoserine (By Similarity).
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way modified and this state
                                                                                                                                                                                                                                                                                                                              EMBL
                                                                                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricuse as long as its content is in no way modified and this stances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Ligase; Lipid
Phosphorylation
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                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Contains 1 ATP-grasp domain.
SIMILARITY: Contains 1 biotin carboxylation domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
SIMILARITY: Contains 1 biotinyl-binding domain.
SIMILARITY: Contains 1 carboxyltransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-grasp.
Biotinyl/lipoyl.
Carboxyltransferase.
ATP (Potential).
By similarity.
Biotin (covalent) (B)
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Phosphoserine (By sin
W; .32886C5D03EEAE0E
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                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ132890; CAB56826.1; -; mRNA.
HSSP; Q00955; 10D4.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
InterPro; IPR011764; BC.
InterPro; IPR001882; Biotin_Carb_C.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR011762; CABC_CT_C.
InterPro; IPR011762; COA_CT_C.
InterPro; IPR011762; COA_CT_C.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR011762; COA_CT_N.
InterPro; IPR05481; CPaSe_D2 ATP_bd.
Pfam; PF02785; Biotin_Carb_C; I.
Pfam; PF01039; Carboxyl_trans; 1.
Pfam; PF02786; CPSase_L_Chain; 1.
PROSITE; PS509189; BIOTINYL LIPOYL; 1.
PROSITE; PS50989; COA_CT_CTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS50980; COA_CT_NTER; 1.
PROSITE; PS00866; CPSASE_2; 1.
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557

630

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phosphate
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                                                                                                                                                                                                                                                                                                                    WCTION: Catalyzes the rate-limiting reaction in the biogenesis long-chain fatty acids. This protein carries three functions tin carboxyl carrier protein, biotin carboxylase, and
                                                                           Biotin
                                                                                                                                                                                                                                            o
                                                                                                    Name=ACACA; Synonyms=ACAC;
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                            STRAIN=Finn-Dorset; TISSUE=Adipose tissue;
MEDLINE=95197015; PubMed=7890176; DOI=10.1016/0378-1119(94)00871
Barber M.C., Travers M.T.;
"Cloning and characterisation of multiple acetyl-CoA carboxylase
                                                                                                                                                                                                                                                                          multiple acetyl-CoA carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                 +
                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                               ATP + biotin-carboxyl-carrier protein carboxybiotin-carboxyl-carrier protein
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                                                                         [Includes
                                                                                                                                                                                                                                                                                                                                                                                = ADP
                                                                                                                                                                                                                                                                                                                                                                                 + HCO(3)(-)
                                                                         alpha)
                         8 (Rel. 36, Created)
5 (Rel. 36, Last sequence update)
5 (Rel. 48, Last annotation update)
carboxylase 1 (EC 6.4.1.2) (ACC-al
2346 AA
                                                                                                                                                                                                                                                                                                                                                                                 + acetyl-CoA
                                                                                                                                                                                                                                                                          n of mul
tissue.
                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                                                                                                                                                               + malonyl-CoA.

CATALYTIC ACTIVITY: A
= ADP + phosphate + c
COFACTOR: Biotin.
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9

Gaps

16

Indels

2346;

Length

DB 1; '.5e-112; les 103;

d. No. 7.5 Mismatches

78;

61.1%; ilarity 63.7%; Conservative

l Similarity 345; Conser

Match

Local

Query Ma Best Loc Matches

Score 1775; Pred. No. 7

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2

377

457

437

510

497

630

557

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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                             VMIKASEGGGGKGIRKCTNGEEFKQLYNAVL
                                                                                                                                                                                             AVFEHMEQCAVKLARMVGYVSAGTVEYLYS-QDGSFYFLELNPRLQVEHPCTEMVADVNL
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                                                                                                                                                                                                                                                   PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTORKPOPQGHVVACRI
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--HVPCPRGHVIAAR
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. 27, Last sequence update)
. 27, Last annotation update)
. 2 (EC 6.4.1.2) (Fragment).
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ dat
EMBL; AJ575431; CAE01470.2; -; mRNA.
GO; GO:0003989; F:acetyl-CoA carboxylase activity
GO; GO:0006524; F:ATP binding; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP GRASP.
InterPro; IPR011764; BC.
InterPro; IPR00089; Biotin lipoyl.
InterPro; IPR005481; CPase L.N.
InterPro; IPR005481; CPase L.N.
InterPro; IPR002114; HPr SerP S.
Pfam; PF02785; Biotin lipoyl;
IPR00364; Biotin lipoyl;
Pfam; PF00289; CPSase L.chain; 1.
Pfam; PF02786; CPSase L.Chain; 1.
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS50975; ATP GRASP; 1.
                                                                                                                                                                                                                                                                     BIOTINYL LIPOYL; 1.
CPSASE 1; UNKNOWN 1.
CPSASE 2; UNKNOWN 1.
PTS HPR SER; UNKNOWN 1
                           LTVSDDVYQQACIHTAEEGLEKAEKIGYP
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PSS0968; BIOTINYL; PS00866; CPSASE 1; PS00867; CPSASE 2;
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QEKE89 HUMAN PRELIMINARY
QEKE89;
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                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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17 618 Biotin carboxylation.

18 466 ATP-grasp.

19 ATP-grasp.

2194 Carboxyltransferase.

2194 ATP (Potential).

1941 By similarity.

2127 Coenzyme A (By similarity).

2129 Coenzyme A (By similarity).

2129 Coenzyme A (By similarity).

2129 Chosphoserine (By similarity).

29 Phosphoserine (By similarity).

29 Phosphoserine (By similarity).
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Biotin (covalent) (By similarity).

Coenzyme A (By similarity).

Coenzyme A (By similarity).

Coenzyme A (By similarity).

Phosphoserine (By similarity).

Phosphoserine (By similarity).

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ATP-grasp domain.
biotin carboxylation domain.
biotinyl-binding domain.
carboxyltransferase domain.
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ed. No. 7.5e-112;
Mismatches 104;
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HSSP; Q00955; 1004.
INTERPRO; IPR011761; ATP GRASP.
INTERPRO; IPR011764; BC.
INTERPRO; IPR0011764; BC.
INTERPRO; IPR0011764; BC.
INTERPRO; IPR000029; Biotin _ lipoyl.
INTERPRO; IPR0011763; CAA CT _C.
INTERPRO; IPR001401; CAA CT _C.
INTERPRO; IPR00139; CAYSABE _D2 ATP_bd.
PROSITE; PSS0979; BC: 1.
PROSITE; PSS0979; BC: 1.
PROSITE; PSS0989; CAA CT _ CTER; 1.
PROSITE; PSS0989; CAA CT _ CTER; 1.
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Matches 345; Conservative
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae
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Peng X.R., Lindgren K., Corneliussen B.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databas:
EMBL; AJ575592; CAE01471.3; -; mRNA.
GO; GO:0009343; C:biotin carboxylase complex; IEA.
GO; GO:0003989; F:acetyl-CoA carboxylase activity; IE.
GO; GO:0004075; F:ATP binding; IEA.
GO; GO:0004075; F:biotin carboxylase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
                           60.9%; Score 1769.5; DB 2; larity 63.4%; Pred. No. 6.4e-112; Conservative 75; Mismatches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.9%; Score 1769.5; DB 2. larity 63.4%; Pred. No. 1.9e-111; Conservative 75; Mismatches 107;
InterPro; IPR011764; BC.

InterPro; IPR00089; Biotin carb C.

InterPro; IPR000089; Biotin lipoyl.

InterPro; IPR010022; Carboxyl trans.

InterPro; IPR011762; COA CT C.

InterPro; IPR011762; COA CT C.

InterPro; IPR011762; COA CT C.

InterPro; IPR005481; CPaSe L N.

InterPro; IPR005481; CpaSe L N.

InterPro; IPR00549; Cphp Synth L D2.

Pfam; PF00364; Biotin carb C; 1.

Pfam; PF00389; Carboxyl trans; 1.

Pfam; PF01039; Carboxyl trans; 1.

Pfam; PF02786; CPSase L Chain; 1.

PROSITE; PS50975; ATP GRASP; 1.

PROSITE; PS50989; COA CT CTER; 1.

PROSITE; PS50989; COA CT CTER; 1.

PROSITE; PS50980; COA CT NTER; 1.

PROSITE; PS50980; COA CT NTER; 1.

PROSITE; PS00866; CPSASE 1; UNKNOWN 1.

PROSITE; PS00866; CPSASE 2; UNKNOWN 1.

PROSITE; PS00866; CPSASE 2; UNKNOWN 1.
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PAAOLOVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKT-ORKPOPOGHVVACR
                                                                                                        QVEHPTTEMVSGVNI
                                                                ITAENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSE
                                                                                                                                                                                                                                                                                                                           Anopheles gambiae str. PEST.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;

Anophelinae; Anopheles.

NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v preliminary data.
EMBL; AAAB01008900; EAA09449.3; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0009374; F:biotin binding; IEA.
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             databases
             DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRL
                                                                                                                                                                                                                                                                             (TrEMBLrel. 26, Created)
(TrEMBLrel. 26, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN=PEST;
The Anopheles gambiae Sequence Committee;
"Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ
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InterPro; IPR011764; BC.
InterPro; IPR001882; Biotin BS.
InterPro; IPR005482; Biotin Carb C.
InterPro; IPR000089; Biotin lipoyl.
InterPro; IPR000022; Carboxyl trans.
InterPro; IPR011763; COA_CT_C.
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011762; COA_CT_N.
005481; CPase_L_N.
005479; Cphp_synth_I
; Biotin_carb_C; 1.
; Biotin_lipoyl; 1.
; Carboxyl_trans; 1.
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_L_chain;
_L_D2; 1.
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ORFNames=ENSANGG0000013173;
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ATP_GRASP;
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BIOTIN;
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IPR011763;
IPR011762;
IPR005481;
IPR005479;
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PSS0979;
PS00188;
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PF00364;
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Q7PQ11;
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01-MAR-2004
01-MAR-2004
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InterPro;
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PROSITE;
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ANOGA
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae
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                                  update)
on update)
                                                                                                                                                                               EMBL; AY382667; AAR37018.1; -; mRNA.
GO; GO:0009343; C:biotin carboxylase complex; IEA.
GO; GO:0009369; F:acetyl-CoA carboxylase activity;
GO; GO:0004075; F:ATP binding; IEA.
GO; GO:0016874; F:biotin carboxylase activity; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR011761; ATP_GRASP.
InterPro; IPR011764; BC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1769.5; DB 2
Pred. No. 1.9e-111;
3; Mismatches 108;
                                                                                                                                                                akil S.J.;
(SEP-2003) to the EMBL/GenBank/DDBJ
                                Last sequence up
Last annotation
(6.4.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOTINYL LIPOYL; 1.
COA CT CTER; 1.
COA CT NTER; 1.
CPSASE 1; UNKNOWN 1.
CPSASE 2; UNKNOWN 1.
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00089; Biotin_lipoyl.
00022; Carboxyl_trans.
011763; COA_CT_C.
011762; COA_CT_N.
005481; CPase_L N.
005479; Cphp_synth_L_D2
02114; HPr_Serp_S.
6 Biotin_carb_C; 1.
7 Biotin_lipoyl; 1.
                       Created)
 PRT;
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CPSase_L_chain;
CPSase_L_D2; 1.
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CPSase_L_Dz,
75; ATP_GRASP; 7
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                     60.9%;
63.5%;
HUMAN PRELIMINARY;
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IPRO00089;
IPRO11763;
IPRO11762;
IPRO05481;
IPRO05479;
IPRO05479;
                                                                          (Human)
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                                                                                                                                         SEQUENCE
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PF01039; Car
PF01039; Car
PF0289; CPS;
PF02786; CPS;
TE; PS50975;
TE; PS50975;
TE; PS50989;
TE; PS50989;
TE; PS50980;
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Best Local Similarity
Matches 345; Conser
                                                                                                                    TaxID=9606;
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                                                                                                                                                 TISSUE=Heart;
Mao J., Wakil
                                                                            Homo sapiens
           06TY48;
05-JUL-2004
                                                                                                                                          NUCLEOTIDE
                                                                Name=ACC2;
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Submitted
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InterPro;
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SEQUENCE
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Q4SCU3;

C Q4SCU3;

T 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

T 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

T 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

T 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

C Chromosome 7 SCAF14650, whole genome shotgun sequence.

S Chromosome 7 SCAF14650, whole genome shotgun sequence.

ORFNames=GSTENG00020334001;

N Tetraodon nigroviridis (Green puffer).

Tetraodon nigroviridis (Green puffer).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Actinopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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1.6e-111;
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1 Similarity 63.3%; Pred. No. 2.64
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Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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,; CAAE01014650; CAG01539.1; -; Genomic_DNA.
ENCE 1267 AA; 141834 MW; 682ADAAE28A169F6
                                                                                                                                                                                                                           Score 1757; DB 2;
Pred. No. 5.5e-111;
69; Mismatches 106;
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                                                                                                 ORFNames=GSTENG00029540001;
ORFNames=GSTENG00029540001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
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Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N. Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Seguren Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bos Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Recha
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data.
EMBL; CAAE01014999; CAG08536.1; -; Genomic_DNA.
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1.1e-108;
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Pred. No. 8.1e
73; Mismatches
   31, Last
31, Last
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ilarity 58.9%;
Conservative 73
13-SEP-2005 (TrEMBLrel. 13-SEP-2005 (TrEMBLrel. 13-Chromosome 12 SCAF14999,
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STRAIN=AX4;

Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,

Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,

Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,

Rankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,

Rethornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

Kerhornou A., Nie X., van Driessehe N., Cronin A., Goodhead I.,

Rathory D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,

Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,

Mardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,

Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,

Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,

A Mardroper A., Sharp S., Simmonds M., Spiegler S., Tivey A.,

A Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,

Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,

Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,

Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;

M. The genome of the social amoeba Dictyostelium discoideum:";
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                                                                                                                                                                                                                                                                                                                        Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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BDBEA99629EE1B2B
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gun (WGS)
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LIKLLETESFRSNEIDTGWLDYLIAEKVQAERPDTMLGI
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Conservative 71; Mismatches 13
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                                                                                                                                                                                                                                                                                      annotation
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EMBL/GenBank/DDBJ whole genome shotgun
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Name=accA; ORFNames=DDB0230067;
Dictyostelium discoideum (Slime
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256733 MW;
GEAPWGDTINFE--DPVCV--
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Q54J08;
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ICE 2282 AA;
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331; Conser
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13-SEP-2005
13-SEP-2005
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                                                     KAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding rat muscle type
                                                                                                            AMGIPLYSIRDIRTLYGM----DPRGNEVIDF-DFSSPESFKTQRKPQPQGHVV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Wistar;
MEDLINE=98322122; PubMed=9655932; DOI=10.1016/S0167-4781(98)000
Abe K., Shinohara Y., Terada H.;
"Isolation and characterization of cDNA encoding rat muscle typacetyl-CoA carboxylase.";
Biochim. Biophys. Acta 1398:347-352(1998).
EMBL; AB004329; BAA25799.1; -; mRNA.
HSSP; Q00955; 10D4.
Ensembl; ENSRNOG0000000658; Rattus norvegicus.
RGD; 620500; Acacb.
             VFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEI
                                                                     MVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERP
                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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GO; GO:0009343; C:biotin carboxylase complex; IEA.
GO; GO:0004075; F:ATP binding; IEA.
GO; GO:0004075; F:Biotin carboxylase activity; IEA.
GO; GO:0004075; F:biotin carboxylase activity; IEA.
GO; GO:0004152; P:metabolism; IEA.
InterPro; IPR011761; ATP GRASP.
InterPro; IPR011764; BC.
InterPro; IPR011764; BC.
InterPro; IPR011763; Carboxyl trans.
InterPro; IPR011763; Carboxyl trans.
InterPro; IPR011763; CAC T.
InterPro; IPR011763; CAP CT N.
InterPro; IPR005419; CPASE L.
InterPro; IPR005419; CPASE L.
InterPro; IPR005419; CPASE L.
InterPro; IPR0289; CAP SARP GRASP; 1.
Pfam; PF00289; CPSASE L. CAPAN; 1.
PROSITE; PS50975; ATP GRASP; 1.
PROSITE; PS50989; COA CT CTER; 1.
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Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                     carboxylase
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01-AUG-1998
01-MAR-2004
Acetyl-CoA c
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Search completed: February Job time: 253 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                       PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQ-PQGHVVACR
                                                                                                                                                       LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES
                                                                                                                                                                                                             LAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD---QG-F
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                                                                                                                             ASP-AEFVTRFGGNRVIETVLIANNGIAAVKWMRSIRRWAYEMFRNERAIRFVVMVTPED
                                                    2456;
                                                                            17;
                                                                           Indels
PS00867; CPSASE 2; UNKNOWN 1.
PS00589; PTS HPR SER; UNKNOWN 1.
2456 AA; 276098 MW; C1D41AF0BEA38863
                                                  Score 1673.5; DB 2;
Pred. No. 6.9e-105;
78; Mismatches 121;
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                                                  57.6%;
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Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDE:

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT FILING DATE: 2003-08-04

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71
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Qy 361 RLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESF 420 I	RESULT 3 US-10-633-835-27 1 US-10-633-835-27 2 Sequence 27, Application US/10633835 2 Publication No. US20040086994A1 3 GENERAL INFORMATION: A APPLICANT: Elitch, Tead D. A APPLICANT: Woltath, Sandra L. A APPLICANT: Weatherly, Stephanie C. TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: NUMBER: US/10/633,835 CURRENT APPLICATION NUMBER: US 60/401,170 PRIOR FILING DATE: 2003-08-05 NUMBER OF SEQ ID NOS: 71 SOFTWARE: Patentin version 3.2 LENGTH: S54 TYPER: PRT ORGANISM: Ustilago maydis FEATURE: NAME/KEY: MISC FEATURE LOCATION: (1) - (554) OTHER INFORMATION: N- and C-terminal deleted Ustilago ACCase BC domain (AAS 4-547) US-10-633-835-27	Query Match 99.1%; Score 2881; DB 4; Length 554; Beef Local Similarity 100.0%; Pred. No. 6.8e-252; Amatches 0; Indels 0; Gaps 0; Amatches 554, O. Indels 0; Indels 0; Gaps 0; Indels 0; Gaps 0; Indels 0; Indels 0; Gaps 0; Indels 0; Indels 0; Gaps 0; Indels Indels
Qy 361 RLQVEHPTTEMVSGVNIPPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESF 420 Db 361 RLQVEHPTTEMVSGVNIPPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESF 420 QY 421 KTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480 Db 421 KTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA 480 QY 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL 540 Db 481 DSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWL 540 QY 541 DGLIQDRLTAERPPADLAV 559 Db 541 DGLIQDRLTAERPPADLAV 559	RESULT 2 US-10-633-835-22 IS-10-633-835-22 Sequence 22, Application US/10633835 Sequence 22, Application US/10633835 Publication No. US20040086994A1 GENERAL INFORMATION: APPLICANT: Biloh, Tedd D. APPLICANT: Weatherly, Stephanie C. TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION OF TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS FILE REFERENCE: 9280.2 FURRENT APPLICATION NUMBER: US/10/633,835 CURRENT FILING DATE: 2003-08-04 PRIOR APPLICATION NUMBER: US 60/401,170 PRIOR APPLICATION NUMBER: US 60/401,170 NUMBER OF SEQ ID NOS: 71 SOFTWARE: PatentIn version 3.2 SEQ ID NO 22 LENGTH: 554 TYPE: PRT ORGANISM: Ustilago maydis FEATURE: NAME/KEY: MISC FEATURE LOCATION: (1)(554) OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC domain (AAS 2-555) US-10-633-835-22	Query Match 99.2‡; Score 2885; DB 4; Length 554; Best Local Simifarity 100.0‡; Pred. No. 2.9-252; 0; Indels 0; Gaps 0; Matches 554; Conservative 0; Mismatches 0; Indels 0;

545

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APPLICANT: Elich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
                                                                             HPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRK
                                              PPPDHKAVSQFIGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKW
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OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC
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Pred. No. 1e-
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/633,8:
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
                                                                                                                                                                                                                  Sequence 23, Application US/10633835 Publication No. US20040086994A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
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Best Local Similarity 100.
Matches 549; Conservative
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ORGANISM: Ustilago maydis
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NAME/KEY: MISC_FEATURE
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SOFTWARE: Pate
SEQ ID NO 23
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-633-835-23
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Pred. No. 4.4e-251;
0; Mismatches 0;
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Sequence 17, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: ACETYL COA CARBOXYLASE

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT FILING DATE: 2003-08-04

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.2

SEQ ID NO 17

LENGTH: 554

TYPE.
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100.0%; Pr
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NAME/KEY: MISC_FEATURE .
LOCATION: (1)...(554)
OTHER INFORMATION: N-terminal.0-633-835-17
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Best Local Similarity 100.
Matches 554; Conservative
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APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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                                             GADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTA
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4.3e-249;
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Pred. No. 4.3
0; Mismatches
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US-10-633-835-28
; Sequence 28, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
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LENGTH: 549
TYPE: PRT
ORGANISM: Ustilago maydis
FEATURE:
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; LOCATION: (1)...(549)
; OTHER INFORMATION: N- ;
US-10-633-835-28
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US-10-633-835-18

Sequence 18, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAIN

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT FILING DATE: 2003-08-04

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
LOCATION: (1). (549)
OTHER INFORMATION: N-terminal deleted Ustilago ACCase
-10-633-835-18
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Pred. No. 4.3e-249;
0; Mismatches 0;
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100.0%; Pr
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Best Local Similarity 100
Matches 549; Conservative
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DGLIQDRLT
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LENGTH: 549
TYPE: PRT
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APPLICANT: Elich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
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Pred. No. 1.4
0; Mismatches
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US-10-633-835-29
; Sequence 29, Application US/1063383!
; Publication No. US20040086994A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; 1
Matches 539; Conservative 0;
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SOFTWARE: Patentin version
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LOCATION: (1)...(539)
OTHER INFORMATION: N- (-10-633-835-29
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ORGANISM: Ustilago m
FEATURE:
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LENGTH: 539
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US-10-633-835-24
Sequence 24, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
APPLICANT: Elich, Tedd D.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDER
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
TITLE OF INVENTION WHBER: US/10/633,835
CURRENT FILING DATE: 2003-08-05
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 539
TYPE: PRT
ORGANISM: Ustilago maydis
FATURE:
FATURE OF WARDING MANDER:
ANAMA CETAL
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LOCATION: (1)..(539)
OTHER INFORMATION: C-terminal deleted Ustilago ACCase BC
0-633-835-24
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Best Local Similarity 100.0%; Pred. No. 2.7e-245;
Matches 539; Conservative 0; Mismatches 0;
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        GENERAL INFORMATION:
APPLICANT: Elich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOF
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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Pred. No. 3.9e-240;
); Mismatches 0;
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US20040086994A1
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LENGTH: 529
TYPE: PRT
ORGANISM: Ustilago maydis
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Best Local Similarity 100
Matches 529; Conservative
                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE;
LOCATION: (1)...(529)
COTHER INFORMATION: C-tous US-10-633-835-25
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                                            Sequence 19, Application US/10633835

Sequence 19, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: ACETYL COA CARBOXYLASE DOMAINS FOR IDE

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: US 60/401,170

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.2
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US-10-633-835-25
; Sequence 25, Application US/10633835
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100.0%; Pr
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LOCATION: (1)..(539)
OTHER INFORMATION: N-terminal
0-633-835-19
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                                   -10-633-835-19
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LENGTH: 539
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Best Local S
Matches 539
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US-10-633-835-30
; Sequence 30, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
nppLICANT: Weatherly, Stephanie C.
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deleted Ustilago ACCase BC

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LUCATION: (1)..(529)
OTHER INFORMATION: N-terminal-10-633-835-20
                   -08-05
    PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2003-08-09
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3
SEQ ID NO 20
LENGTH: 529
TYPE: PRT
ORGANISM: Ustilago maydis
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NAME/KEY: MISC |
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Pred. No. 9e-240;
0; Mismatches 0;
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBO TITLE OF INVENTION: ACETYL COA CARBOXYLASE FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARE
TITLE OF INVENTION: ACETYL COA CARBOXYLASE
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
                                                                                                                                                                                  C-terminal
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Publication No. US20040086994A1
GENERAL INFORMATION:
                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; P
Matches 529; Conservative 0;
                                                                                                                                                       NAME/KEY: MISC_FEATURE LOCATION: (1): (529)
OTHER INFORMATION: N- and 0-633-835-30
                                                                                                                                ORGANISM: Ustilago maydis
                                                                                              SEQ ID NO 30
LENGTH: 529
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US-10-633-835-20
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NAME/KEY:
LOCATION:
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US-10-633-835-26
; Sequence 26, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 26
            529
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            Length
; DB 4; Lr
1.1e-239;
- 0;
         Score 2746; D
Pred. No. 1.1
0; Mismatches
         Query Match
Best Local Similarity 100.0%; P
Matches 529; Conservative 0;
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SOFTWARE: PatentIn version
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ORGANISM: Ustilago maydis
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; LOCATION: (1)..(519)
; OTHER INFORMATION: N
US-10-633-835-31
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Sequence 31, Application US/10633835

Bublication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS;

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT APPLICATION NUMBER: US 60/401,170

PRIOR APPLICATION NUMBER: US 60/401,170

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.2
                                                                                 519
                                                                                                   Indels
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                                 NAME/KEY: MISC_FEATURE
LOCATION: (1). (519)
OTHER INFORMATION: C-terminal deleted Ustilago ACCase
-10-633-835-26
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       TYPE: PRT
ORGANISM: Ustilago maydi
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LENGTH: 519
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APPLICANT: Elich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
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deleted Ustilago ACCase
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                                               Score 2698; DB 4;
Pred. No. 2.4e-23;
; Mismatches 0
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                                               Query Match
Best Local Similarity 100.0%;
Matches 519; Conservative
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OTHER INFORMATION: N-terminal
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IDENTIFICATION
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                                         HKIADHFIGGNRLENAPPSKVKEWVAAHDGHTVITNVLIANNGIAAVKEIRSVRKWAYET
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APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
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; LOCATION: (1)...(581)
; OTHER INFORMATION: N-terminal
US-10-633-835-52
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SOFTWARE: Patentin ver
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Publication No. US20
GENERAL INFORMATION:
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Sequence 53, Application US/10633835;
Publication No. US20040086994A1;
GENERAL INFORMATION:
APPLICANT: Elich, Tedd D.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDE;
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS;
FILE REFERENCE: 9280.2;
FURRENT APPLICATION NUMBER: US/10/633,835;
CURRENT FILING DATE: 2003-08-04;
PRIOR PILING DATE: 2003-08-05;
NUMBER OF SEQ ID NOS: 71;
SOFTWARE: Patentin version 3.2
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OTHER INFORMATION: N-terminal deleted Magnaporthe ACCase-10-633-835-53
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     red. No. 5.6e-2
Mismatches
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     Pred
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  Local Similarity 100.0% nes 519; Conservative
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ORGANISM: Magnaporthe grisea
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ENGTH: 571
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3698
LENGTH: 2301
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
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Hinkle, Gregory
Slater, Steven C
Goldman, Barry S
Chen, Xianfeng
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OTHER INFORMATION: unsure
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Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDE

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT FILING DATE: 2003-08-04

PRIOR PILING DATE: 2003-08-05

PRIOR FILING DATE: 2003-08-05
         NGEEFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDC
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larity 73.5%; Pred. No. 9.9e-187;
Conservative 59; Mismatches 88;
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SOFTWARE: PatentIn version 3.2
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APPLICANT: Volrath, Sandra L.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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NAME/KEY: MISC FEATURE

LOCATION: (1)...(571)

OTHER INFORMATION: C-terminal
US-10-633-835-55
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ORGANISM: Magnaporthe grisea
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US-10-633-835-55
; Sequence 55, Applicat:
; Publication No. US200,
; GENERAL INFORMATION:
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LENGTH: 571
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Sequence 54, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Blich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: ACETYL COA CARBOXYLASE DOMAINS FOR IDER

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

TITLE OF INVENTION NUMBER: US/10/633,835

CURRENT APPLICATION NUMBER: US 60/401,170

PRIOR APPLICATION NUMBER: US 60/401,170

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.2
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 NNNYANVDLIVDVAERAGVHAVWAGW
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; LOCATION: (1)...(581)
; OTHER INFORMATION: C-te
US-10-633-835-54
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ORGANISM: Magnaporthe
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US-10-633-835-54
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KFAQAFQQVLDELPGSPVFVMKLAGQARHLEVQILADQYGNNISLFGRDCSVQRRHQKII
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Pred. No. 9.6e-
5; Mismatches
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APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBC
TITLE OF INVENTION: ACETYL COA CARBOXYLASE
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
LENGTH: 521
                                                                                                                                                                                                                                                                                                        Sequence 64, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
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US-10-633-835-64
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Best Local Similarity
Matches 391; Conser
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; Sequence 2130, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2130
; LENGTH: 2241
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Sequence 34, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Blich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT PILING DATE: 2003-08-04

PRIOR PILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SEO TWANTE: PatentIn version 3.2
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70.9%; Score 2060; DB 4;
Best Local Similarity 69.1%; Pred. No. 2e-177;
Matches 386; Conservative 76; Mismatches 89;
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LOCATION: (1)...(570)
OTHER INFORMATION: N-terminal
OTHER INFORMATION: 12-581)
0-633-835-34
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ORGANISM: Saccharomyces
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Pred. No. 2e-177;
76; Mismatches 89;
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US-10-633-835-35

Sequence 35, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYI

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INF

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: US 60/401,170

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.2

LENGTH: 560

TYPE: PRT
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; LOCATION: (1)...(560)
; OTHER INFORMATION: N-terminal
; OTHER INFORMATION: 22-581)
US-10-633-835-35
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APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
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Pred. No. 2.1e-177
5; Mismatches 89
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.2
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US-10-633-835-8
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APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMITITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS FILE REFERENCE: 9280.2
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                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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Sequence 33, Application US/1063383
Publication No. US20040086994A1
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LOCATION: (1): [(575)
OTHER INFORMATION: N-terminal
OTHER INFORMATION: 7-581)
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APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAIN;
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS;
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
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     DSOFGHIFAYGADRSEARKOMVISLKELSIRGDFRT
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                                                                                                          US-10-633-835-36
; Sequence 36, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
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                                            DGLIQDRLTAERPPADLAV
                                                       ; LOCATION: (1)...(550)
; OTHER INFORMATION: N-terminal
; OTHER INFORMATION: 32-581
US-10-633-835-36
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larity 69.7%;
Conservative
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SEQ ID NO 36
LENGTH: 550
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1998
LENGTH: 2233
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                                                                                                                                                         Sequence 1998, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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APPLICANT: Elich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDENTIFICATION
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
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Pred. No. 1.3e-176;
5; Mismatches 86;
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                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Sąccharomyces cerevisiae
                                                                                                              Sequence 44, Application US/1063383 Publication No. US20040086994A1 GENERAL INFORMATION:
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ilarity 69.3%;
Conservative 76
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OTHER INFORMATION: N- and
OTHER INFORMATION: domain
-10-633-835-44
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Best Local Similarity
Matches 383; Conser
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NAME/KEY: MISC
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APPLICANT: Elich, Tedd D.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDE
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 32
LENGTH: 580
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Pred. No. 7.4e-177
6; Mismatches 90
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Sequence 32, Application US/1063383:
Publication No. US20040086994A1
GENERAL INFORMATION:
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LOCATION: (76)...(76)
OTHER INFORMATION: Saccharomyces
0-633-835-32
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Best Local Similarity 68.9%;
Matches 385; Conservative 7
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APPLICANT: Elich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 575;
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Pred. No. 1.4e-176;
6; Mismatches 86;
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CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(575)
OTHER INFORMATION: N- and C-terminal
OTHER INFORMATION: domain (AAS 4-578)
0-633-835-43
                                                                                                                            Sequence 43, Application US/10633835
Publication No. US20040086994A1
GENERAL INFORMATION:
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.l Similarity 69.3%; P1
383; Conservative 76;
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PatentIn version
                                          DGLIQDRLTAERP
                                                        TYPE: PRT
ORGANISM: Saccharomyces
                                                                                                    RESULT 34
US-10-633-835-43
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                                                                                                                                                          APPLICANT: Elich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Volrath, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS FILLE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR PILING DATE: 2003-08-05
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Pred. No. 1.4e-176
5; Mismatches 86
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                                                                                                                         Application US/1063383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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OTHER INFORMATION: C-terminal
OTHER INFORMATION: 2-576)
10-633-835-38
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nilarity 69.3%;
Conservative 76
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SOFTWARE: PatentIn version
SEQ ID NO 38
LENGTH: 575
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DDLITHKMTAEKP
                                     DGLIQDRLTAERP
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hes 383; Conser
                                                                                                                         Sequence 38, Applica
Publication No. US20
GENERAL INFORMATION:
                                                                                                 SULT 33
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FEATURE:
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                                                      US-10-633-635-37

US-10-633-635-37

US-10-633-635-37

Sequence 37, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Blich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT APPLICATION NUMBER: US 60/401,170

PRIOR APPLICATION NUMBER: US 60/401,170

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn version 3.2
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1 Similarity 70.5%; Pred. No. 7.3e-176;
380; Conservative 74; Mismatches 82;
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CTHER INFORMATION: N-terminal
CS-10-633-835-37
                                                                                                                                                                                                                                               SEQ ID NO 37
LENGTH: 540
TYPE: PRT
ORGANISM: Saccharomyces
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NAME/KEY: MISC_FEATURE
LOCATION: (1)...(540)
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                                                                                                              Sequence 65, Application US/10633835
; Sequence 65, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDE
TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; FILE REFERENCE: 9280.2
; CURRENT APPLICATION NUMBER: US/10/633,835
; CURRENT FILING DATE: 2003-08-04
; PRIOR PILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 65
; LENGTH: 511
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Pred. No. 3.2e-176;
55; Mismatches 72;
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Best Local Similarity 75.1%;
Matches 384; Conservative
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NAME/KEY: MISC_FEATURE
LOCATION: (1)..(511)
OTHER INFORMATION: N- and C-
OTHER INFORMATION: 72-582)
                                                          572
                                   DGLIQDRLTAERP
                                                DDLITHKMTAEKP
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US-10-633-835-39
; Sequence 39, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Blich, Tedd D.
; APPLICANT: Weatherly, Stephanie C.
; TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR IDER
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
; CURRENT APPLICATION NUMBER: US 60/401,170
; PRIOR APPLICATION NUMBER: US 60/401,170
; PRIOR FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
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Best Local Similarity 69.2%; Pred. No. 5.7e-175; Matches 380; Conservative 75; Mismatches 86;
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                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE
LOCATION: (1)..(570)
OTHER INFORMATION: C-terminal
OTHER INFORMATION: 2-571)
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                                         APPLICANT: Elich, Tedd D.
APPLICANT: Volrath, Sandra L.
APPLICANT: Volrath, Sandra L.
APPLICANT: Weatherly, Stephanie C.
TITLE OF INVENTION: RECOMBINANT BIOTIN CARBOXYLASE DOMAINS FOR TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS
FILE REFERENCE: 9280.2
CURRENT APPLICATION NUMBER: US/10/633,835
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 60/401,170
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.2
SEQ ID NO 45
LENGTH: 560
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
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Pred. No. 5.6e-175;
75; Mismatches 86;
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RESULT 37
US-10-633-835-45
; Sequence 45, Application US/10633835
; Publication No. US20040086994A1
; GENERAL INFORMATION:
; APPLICANT: Elich, Tedd D.
; APPLICANT: Volrath, Sandra L.
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Best Local Similarity 69.2%;
Matches 380; Conservative
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LOCATION: (1)..(560)
OTHER INFORMATION: N- and
OTHER INFORMATION: domain
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Best Local Similarity 75.4%;
Matches 378; Conservative
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NAME/KEY: misc feature
OTHER INFORMATION: N- and
OTHER INFORMATION: 72-572)
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                                                                                                                                                                TYPE: PRT
ORGANISM: Magnaporthe
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LOCATION: (1)...(550)
OTHER INFORMATION: N- and C-terminal deleted Saccharomyces
OTHER INFORMATION: domain (AAS 17-566)
0-633-835-46
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US-10-633-835-46

Sequence 46, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: ACETYL COA CARBOXYLASE DOMAIN

TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: US 60/401,170

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.2
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Best Local Similarity 69.7%; Pred. No. 2.3e-174;
Matches 379; Conservative 73; Mismatches 84;
                                                                                                                                                                        ORGANISM: Saccharomyces cerevisiae
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US-10-633-835-66

Sequence 66, Application US/10633835

Sequence 66, Application US/10633835

Publication No. US20040086994A1

GENERAL INFORMATION:

APPLICANT: Elich, Tedd D.

APPLICANT: Weatherly, Stephanie C.

TITLE OF INVENTION: ACETYL COA CARBOXYLASE DOMAINS FOR TITLE OF INVENTION: ACETYL COA CARBOXYLASE INHIBITORS

FILE REFERENCE: 9280.2

CURRENT APPLICATION NUMBER: US/10/633,835

CURRENT APPLICATION NUMBER: US 60/401,170

PRIOR FILING DATE: 2003-08-05

NUMBER OF SEQ ID NOS: 71

SOFTWARE: Patentin version 3.2
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Pred. No. 7.1e-174;
; Mismatches 69;
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88029 hits satisfying chosen parameters: of number Total

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Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Database

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/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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No. is the number of results predicted by chance to have greater than or equal to the score of the result being partived by analysis of the total score distribution. score gand is Pred.

	Description	Sequence 14, Appl	equence 16	equence 4	equence 13	6	4	11,	8, 7	10,	2,	710,	1642	1317	2448	12,	13,	208,	218,		648,	1654	370,	1002,	368, A	1
SUMMARIES		US-11-186-999-14	US-11-186-999-16		US-11-186-999-13	1	66-9	σ	-666-9	66-9	σ	-10-995-56	-10-46	-10-821-234-131	-10-793-626-2	-10-85	-730-1	-858-730-2	-21	3-626-80	3-62	US-10-467-657-1654	US-11-055-822-370	US-11-055-822-1002	US-11-055-822-368	US-11-055-822-1000
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ALIGNMENTS

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RESULT 1 US-11-186-999-14 ; Sequence 14, Application US/11186999 ; Publication No. US20060019364A1 ; GENERAL INFORMATION: ; APPLICANT: Bristol-Myers Squibb Company ; TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2 SEQUENCES AND METHODS ; FILE REFERENCE: BMS Docket Number 10245 NP ; CURRENT APPLICATION NUMBER: US/11/186,999	FILLING DAIE: F SEQ ID NOS: 14 2455 PRT IM: Rattub nor

Gaps 2455; 17; Length Indels 7; Score 1777.5; DB 7 Pred. No. 2.5e-131; ; Mismatches 107; Ouery Match
Best Local Similarity 63.4%; Pr
Matches 344; Conservative 75;

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Pred. No. 2.5e-131;
75; Mismatches 107;
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Publication No. US20060019364A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: ACETYL COA CARBOXYLASE;
FILE REFERENCE: BMS Docket Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999;
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
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Best Local Similarity 63.4
Matches 344; Conservative
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APPLICANT: Kan, Zhengyan
APPLICANT: Garrett-Engele, Philip W.
APPLICANT: Armour, Christopher D.
APPLICANT: Raymond, Christopher K.
APPLICANT: Castle, John C.
TITLE OF INVENTION: ALTERNATIVELY SPLICED ISOFORM OF
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE 2 (ACC2)
FILE REFERENCE: RS0220
CURRENT APPLICATION NUMBER: US/11/144,368
CURRENT APPLICATION NUMBER: 60/577,234
PRIOR FILING DATE: 2004-06-04
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Pred. No. 9.6e-131;
5; Mismatches 107;
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Sequence 4, Application US/11144368
Publication No. US20050272082A1
GENERAL INFORMATION:
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Best Local Similarity 63.4%;
Matches 344; Conservative
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SEQUENCES AND METHODS

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APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: ACETYL COA CARBOXYLASE FILE REFERENCE: BMS Docket Number 10245 NP

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Pred. No. 1.1e-130;
5; Mismatches 107;
US-11-186-999-13
; Sequence 13, Application US/11186999
; Publication No. US20060019364A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2
; FILE REFERENCE: BMS Docket Number 10245 NP
; CURRENT APPLICATION NUMBER: US/11/186,999
; CURRENT FILING DATE: 2005-07-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.2
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US-11-186-999-6
; Sequence 6, Application US/11186999
; Publication No. US20060019364A1
; GENERAL INFORMATION:
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Best Local Similarity 63.4%;
Matches 344; Conservative
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ORGANISM: Homo sapiens
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Publication No. US20060019364A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: ACETYL COA CARBOXYLASE
FILE REFERENCE: BMS Docket Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
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; ORGANISM: Homo
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; ORGANISM: HOMO
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Pred. No. 3.9e-123;
3; Mismatches 121;
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Publication No. US20060019364A1;
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2;
FILE REFERENCE: BMS Docket Number 10245 NP;
CURRENT APPLICATION NUMBER: US/11/186,999;
CURRENT FILING DATE: 2005-07-21
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Best Local Similarity 60.3
Matches 327; Conservative
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SOFTWARE: Patentin ver
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Score 1739; DB 7;
Pred. No. 2.7e-128;
5; Mismatches 107;
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TITLE OF INVENTION: ACETYL COA CARBOXYLASE
FILE REFERENCE: BMS Docket Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
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LOCATION: (1)..(2458)
OTHER INFORMATION: Xaa is any amino acid
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Publication No. US20060019364A1
GENERAL INFORMATION:
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Pred. No. 8.1e-123;
); Mismatches 117;
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Publication No. US20060019364A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: ACETYL COA CARBOXYLASE 2
FILE REFERENCE: BMS Docket Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
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Pred. No. 3.9e-123;
3; Mismatches 121;
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Publication No. US20060019364A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: ACETYL COA CARBOXYLASE;
FILE REFERENCE: BMS Docket Number 10245 NP
CURRENT APPLICATION NUMBER: US/11/186,999;
CURRENT FILING DATE: 2005-07-21
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 2456
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                                                                                                       Sequence 710, Application US/10995561
Sequence 710, Application US/10995561
Sequence 710, Application US/2054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 3.3e-117;
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TYPE: PRT
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Pred. No.
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2001-02-12
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Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
Sequence 1642, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION: APPLICANT: CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
                                                                                                                                                                                                                                                                                                                             version 1.04
                                                                                                                                                                                                                                                                                                                                                                                                                  gonorrhoeae
                                                                                                      APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL
FILE REFERENCE:
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l Similarity 31.9%;
168; Conservative 92
                                                                                        FONTANA Maria Rita
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PRIOR FILING DATE: 2001-02
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RIGYRGAGTFEFLY
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ID NO 1642
ENGTH: 453
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
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Pred. No. 1.1e-42;
87; Mismatches 178;
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis
FILE REFERENCE: 821A
                                                   CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
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; Sequence 2448, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
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QAMGDKIESKLLAKKAEVNTIP-
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il Similarity 31.8%;
166; Conservative 8
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SOFTWARE: Patentin Ver.
EQ ID NO 2448
LENGTH: 1151
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SEQ ID NO 1317
LENGTH: 703
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SEQ ID NO 2
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                                                         synthetic
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                                                                                                                                                          Indels
                                                                                                                        Length
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                                                      Sequence:
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                                                                                                                     core 625; DB 6;
red. No. 3.7e-41;
Mismatches 182;
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APPLICANT: Driggers, Edward M.
APPLICANT: Madden, Kevin T.
APPLICANT: O'Leary, Jessica
APPLICANT: O'Toole, George
APPLICANT: Trueheart, Joshua
APPLICANT: Walbridge, Michael J.
APPLICANT: Yorgey, Peter S.
TITLE OF INVENTION: PRODUCTION
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: ||| :| :: | | | :: | EMRIRG-VKTNIPFLINVMRNDKFRSGDYTTKFIE
                                                    n of Artificial sequence
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116 HLDMFGDKVKARTTAINANLPVIP--GT--
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CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
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                                                                                                                      Score
Pred.
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Publication No. US20050255568A1
GENERAL INFORMATION:
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Blomquist, Paul
Doten, Reed
Driggers, Edward M.
Madden, Kevin T.
O'Leary, Jessica
O'Toole, George
Trueheart, Joshua
Walbridge, Michael J.
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                                                   Description amino acid a
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TYPE: PRT
ORGANISM: Artificial Sequence
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8 IKKLLVANRGEIAIRIFRA
                                                                                                                    Query Match
Best Local Similarity 31.8%;
Matches 164; Conservative
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  ; TYPE: FK1
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: D
; OTHER INFORMATION: a
US-10-793-626-2448
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OF SEQ ID NOS: 364
SOFTWARE: FastSEQ 1
SEQ ID NO 13
LENGTH: 1127
TYPE: PRT
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                                                                                      Query Match
Best Local S
Matches 162
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                                                                                       Length 1124;
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: 14184-030001
                                                                                                                Indels
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Pred. No. 5.3e-37;
87; Mismatches 199;
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CURRENT APPLICATION NUMBER: US/10/858,73
CURRENT FILING DATE: 2004-06-01
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 Version
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                                                  ; ORGANISM: Streptomyces coelicolor
US-10-858-730-12
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O'Leary, Jessica
O'Toole, George
Trueheart, Joshua
Walbridge, Michael J.
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FastSEQ for Windows
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                                                                                      Query Match
Best Local Similarity 30.8%;
Matches 161; Conservative
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SOFTWARE: F
SEQ ID NO 12
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1.1e-36;
ches 196;
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                                                                                                                     Score 568; DB
Pred. No. 1.1e
8; Mismatches
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                                                  , ORGANISM: Mycobacterium smegmatis
US-10-858-730-13
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APPLICANT: Yorgey, Peter S.
TITLE OF INVENTION: METHODS AND
                                                                                                                                                                                                              PRODUCTION
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Walbridge, Michael
Yorqey, Peter S.
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2003-05-30
NUMBER: US 60
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Madden, Kevin T.
O'Leary, Jessica
O'Toole, George
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PRIOR FILING DATE: 2003-0:
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                                                                                     Length 1140;
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188;
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Pred. No. 9.5e-
90; Mismatches
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDER
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 218
LENGTH: 341
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 Version
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Sequence 218, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
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al Similarity 29.3%;
157; Conservative 5
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31.7%;
                                            ; ORGANISM: Coryne-bacterium US-10-858-730-208
for
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LENGTH: 1140
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                                              - | : :: : [:|||||||||| - EGLIQSIDDAKKIAKKIGYPVIIKATAG
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                                                                                                      YVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGP
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..4e-32;
les 184;
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Pred. No. 1.4e
35; Mismatches
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMII
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
                                                                                     GGGKGIRKCTNGEEFKQLYNAVLGEVP--
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1 Similarity 27.7%;
144; Conservative 95
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Conservative
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ORGANISM: Artificial
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SEQ ID NO 804
LENGTH: 453
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Qy 471 GTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKELSIRGDFRTT :	-1654 54, Applic No. US20 ORMATION: CHIRON SI FONTANA	APPLICANT: PIZZA Mariagrazia APPLICANT: MASIGNANI Vega APPLICANT: MONACI Elisabetta TITLE OF INVENTION: GONOCOCCAL PROTEINS FILE REFERENCE:	CURKENT APPLICATION NUMBER: US/10/46/,65/ CURRENT FILING DATE: 2003-08-11 PRIOR APPLICATION NUMBER: GB-0103424.8 PRIOR FILING DATE: 2001-02-12 NUMBER OF SEQ.ID NOS: 9218 SOFTWARE: SeqWin99, version 1.04 SEQ ID NO 1654 LENGTH: 1071 TYPE: PRT CORGANISM: Neisseria gonorrhoeae US-10-467-657-1654	Query Match Query Match Best Local Similarity 21.8%; Pred. No. 4.9e-06; Matches 79; Conservative 66; Mismatches 162; Indels 56; Gal Qy 211 HTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPV DD 150 HTMNEALAAQEQVGFPTLIRPSFTMGGSGGGIAYNKDEFLAICERGFDASPTHEL	Qy 269 KLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEA-PVTIAPEDA: : ::: : : : : :	Qy 382 LQVAMGIPLYSIR-DIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVA 	Oy 438 TAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADR :	Qy 498 RKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTA 	Oy 554 PAD 556 : Db 471 VSD 473	RESULT 22 US-11-055-822-370 ; Sequence 370, Application US/11055822 ; Publication No. US20050260707A1 ; GENERAL INFORMATION: ; APPLICANT: Pompejus, Markus ; APPLICANT: Kroger, Burkhard
Qy 271 AGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRL 330 : : : : : : : : :	QY 391 YSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGM 450 : ; ; ; ; ; ; ; ; ;	OY 505 LKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLD 541 : :: : : : : : : :	3-626-648 2e 648, Application US/107936 ation No. US20050255478A1 CANT: KIMMERLY, WILLIAM JOHN OF INVENTION: STAPHYLOCOCCUS REFERENCE: PU3480US AT APPLICATION NUMBER: US/10/ AT FILING DATE: 2004-03-04	PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-11 NUMBER OF SEQ ID NOS: 4472 SOFTWARE: Patentin Ver. 2 SEQ ID NO 648 LENGTH: 309 TYPE: PRT ORGANISM: Artificial Sequences	; realons: ; oTHER INFORMATION: Description of Artificial Sequence: synthetic ; OTHER INFORMATION: amino acid sequence ; FEATURE: ; NAME/KEY: MOD_RES ; LOCATION: (309) ; OTHER INFORMATION: variable amino acid US-10-793-626-648	Query Match Best Local Similarity 31.8%; Pred. No. 3.9e-31; Matches 117; Conservative 53; Mismatches 108; Indels 90; Gaps 7;	Oy 175 ADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEG 234 : :	Qy 235 GGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAI 290 :: :: ::	Qy 291 SIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPES 350 : :: :: : : :	OY 351 GEFAFLELNPRLQVEHPTTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVI 410 : : :

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Gaps 15;
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HELLIE 207
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EDKAEI 419
RITVE 519
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175;
                           CANT: Haberhauer, Gregor
OF INVENTION: CORYNEBACTERIUM GLUTAMICUM OF INVENTION: METABOLIC PATHWAY PROTEINS
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Pred. No. 3.5e-0
69; Mismatches 1
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                                                  FILE REFERENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 1158
                                                                                                                                                                                                                                                      FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931418.7
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931419.5
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931420.9
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2000-06-23
                                                                                                                                                               FILING DATE: 1999-08-12
APPLICATION NUMBER: 60/187 070
FILING DATE: 1999-08-12
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FILING DATE: 1999-06-25
APPLICATION NUMBER: 60/142,101
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                                                                                   2005-02-
                                                                                                                                                                                                      FILING DATE: 2000-03-09
APPLICATION NUMBER: DE 1
FILING DATE: 1999-07-01
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APPLICATION NUMBER: 60/
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Schroder, Hart
Zelder, Oskar
Haberhauer, Gr
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FILING DATE: 2000-0
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Best Local Similarity
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Mismatches 17
                                                                             CORYNEBACTERIUM GLUTAMICUM METABOLIC PATHWAY PROTEINS
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R APPLICATION NUMBER: 60/148,613

R FILING DATE: 1999-08-12

R APPLICATION NUMBER: 60/187,970

R FILING DATE: 2000-03-09

R FILING DATE: 1999-07-01
                                                                                                                               US/11/055,822
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APPLICATION NUMBER: DE 19921110
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FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931418
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                                                                                                                                                2000-06-23
                                                                                                                                                                                                60/141,031
                                                                                                                                                                                                                             APPLICATION NUMBER: 60/142,101
                                           APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
IITLE OF INVENTION: CORYNEBACTERIUM
ITLE OF INVENTION: METABOLIC PATHY
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                                                                                                                                                                         FILING DATE: 2000-06-23
APPLICATION NUMBER: 60/
FILING DATE: 1999-06-25
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ing Prior Application d
OF SEQ ID NOS: 1158
              Burkhard
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NO 1002
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92; Conserv
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US-11-055-822-1002 ; Sequence 1002, Application US/11055822 ; Publication No. US20050260707A1

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                                                                                                                    CORYNEBACTERIUM GLUTAMICUM GENES ENCODING METABOLIC PATHWAY PROTEINS
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Pred. No. 3.8e-05;
59; Mismatches 175;
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                                                                                                                                                                  US/11/055,822
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APPLICATION NUMBER: DE 19931418.7
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931419 E
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PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data remove
NUMBER OF SEQ ID NOS: 1158
                                                                                                                                                                                                                                R FILING DATE: 1999-06-25
R APPLICATION NUMBER: 60/142,101
R FILING DATE: 1999-07-02
R APPLICATION NUMBER: 60/148,613
R PILING DATE: 1999-08-12
R APPLICATION NUMBER: 60/187,970
R FILING DATE: 2000-03-09
R APPLICATION NUMBER: DE 19930476.
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                                                                                                                                                                                                                                                                                                                                      DE 19930476
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1-055-822-368
                                                                                                                                                 FILE REFERENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/05:
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
           Application US/11055822 US20050260707A1
                                                                                                                                                                                                                      60/141,031
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                                                                Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
                                                                                                                                                                                                          FILING DATE: 2000-06 APPLICATION NUMBER:
                                                                                                           Haberhauer,
                                                    Pompejus,
                                                                                                                     OF INVENTION:
                                                                                                                                       INVENTION:
         Sequence 368, Application No. US2 GENERAL INFORMATION
-11-055-822-368
                                                                              APPLICANT:
APPLICANT:
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ed. No. 3.8e-05;
Mismatches 175
                                                                                                                                                                                                                                                                                               METABOLIC PATHWAY PROTEINS
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                                                                                                                         APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR APPLICATION NUMBER: 60/187,970

DR FILING DATE: 2000-03-09

DR APPLICATION NUMBER: DE 19930476.9

DR FILING DATE: 1999-07-01

DR APPLICATION NUMBER: DE 19931415.2

DR FILING DATE: 1999-07-08

DR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                            FILE REFERENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
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Sequence 1000, Application US/11055822 Publication No. US20050260707A1 GENERAL INFORMATION:
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655 IVQLG--GQTPLGLADRL-
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                                                                                                                                                         APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CPCN
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Mismatches
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ENT APPLICATION NUMBER: US/11/055,822
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US-11-055-822-910,
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/606,740 FILING DATE: 2000-06-7-7
                                                                                                 Application US/11055822
. US20050260707A1
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1999-06-25
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FILING DATE: 2000-03-09
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PRIOR APPLICATION NUMBER: DE 199
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 199
PRIOR APPLICATION NUMBER: DE 199
PRIOR APPLICATION NUMBER: DE 199
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application date
NUMBER OF SEQ ID NOS: 1158
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/
FILING DATE: 1999-07-02
APPLICATION NUMBER: 60/
FILING DATE: 1999-08-12
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                                                                                  Sequence 910, Applica
Publication No. US200
GENERAL INFORMATION:
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90; Conser
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Best Local S
Matches 90
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/195792
PRIOR APPLICATION NUMBER: 09/839446
149 IIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQA
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                                                                             | : : | | : : | | : : | 318 LGLPVDVTLISPGASAVIYGGIESEGVSYTGLABALAVAETDLRIFAKPBAFTKRR
                                                                                                                                                                             Sequence 3294, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial; OTHER INFORMATION: amino acid sequence US-10-793-626-3294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101.5; Pred. No. 1.1; Mismatches
                                                    LOVAMGIPLYSIRDIRTLY-GMDPRGNE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1010, Application US/10453372
Publication No. US20060003323A1
GENERAL INFORMATION:
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larity 24.6%;
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial
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Best Local Similarity
Matches 34; Conser
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LENGTH: 371
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APPLICATION NUMBER:

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                                                                          7;
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                                                                         98.5;
No. 15;
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                                                                         Score
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APPLICANT: Hucul, John
APPLICANT: Haltli, Bradley A.
APPLICANT: Wagenaar, Melissa
APPLICANT: Graziani, Edmund
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Kulowski, Kerry
Pong, Kevin
 ; LENGTH: 1579
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-052-554A-9
                                                                                                      Conservative
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                                                                                    l Similarity
125; Conser
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Publication No. US20050288866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDITITLE OF INVENTION: PROTEINS OF THERAPEUTIC POFILE REFERENCE: 30853/40359A;
CURRENT APPLICATION NUMBER: US/11/052,554A;
CURRENT FILING DATE: 2005-02-07;
PRIOR APPLICATION NUMBER: US 60/589,227
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PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed:
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
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SOFTWARE: Patentin version
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                                                                                                                                                                               Gaps
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; Sequence 3314, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PRO:
; FILE REFERENCE: PU3480US
; FILE REFERENCE: 2004-03-04
; FILE REPERENCE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3314
; LENGTH: 230
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                                                                                                                                                                            Mismatches
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                                                                                                                                                  Score 97.5;
Pred. No. 4
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Pred. No. 1
                 576,89
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PRIOR FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2004-06-03
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.3
                                                                                                                                                 3.4%;
ilarity 21.7%;
Conservative
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US-11-143-980-50
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ORGANISM: Artificial
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Best Local Similarity
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ENGTH: 3073
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                                                                                                       GYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLA
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                                   DKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQQACIHTAEEGLEKAEKI
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                                                                      -SFLRSEYEKYENNIIKLVN-
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CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
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; Sequence 316, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
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JATE: 2001-02-12
JETWARE: SegWin99, version 1
LENGTH: 717
TYPE: PT
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FONTANA Maria Rita
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APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
Conservative
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OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                Score 96; DB Pred. No. 3.2;
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                          APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629WO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
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FILE REFERENCE: 14114.0373U2
CURRENT APPLICATION NUMBER: US/10/519,531
CURRENT FILING DATE: 2004-12-27
PRIOR APPLICATION NUMBER: PCT/US03/20325
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392,630
PRIOR FILING DATE: 2002-06-27
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larity 19.3%; Pred. No.
Conservative 55; Mismatc
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             Biosynexus Incorporated
of Sheffield
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Publication No. US20050244429A1
GENERAL INFORMATION:
APPLICANT: Folks, Thomas M.
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ENGTH: 512
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LENGTH: 393
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TITLE OF INVENTION: LIVE REPLICATING SPUMAVIRUS VECTILE REFERENCE: 14114.0373U2
CURRENT APPLICATION NUMBER: US/10/519,531
CURRENT APPLICATION NUMBER: PCT/US03/20325
PRIOR APPLICATION NUMBER: 60/392,630
PRIOR FILING DATE: 2002-06-27
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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Similarity 19.3%;
88; Conservative 55
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-519-531-5
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CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US/10/212,219
PRIOR FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US 60/316,276
PRIOR FILING DATE: 2001-09-04
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Publication No. US20050266536A1
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APPLICANT: HERMANN, THOMAS
APPLICANT: MORBACH, SUSANNE
APPLICANT: KRAEMER, REINHARD
TITLE OF INVENTION: PROCESS FOR TI
TITLE OF INVENTION: CORYNEFORM BI
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ilarity 20.9%;
Conservative 59
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Best Local Similarity
Matches 102; Conser
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GENERAL INFORMATION
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    --MTETLLVQNANPDC
                           SDDVYQQACIHTAEFGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGFEFKQLYNAVLGEV
                                                                                          --HQKIIEEA
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RMYSPTSILDIRQGPKEPPRDYVDRFYKTLRAEQASQEVKNW-
                                                                                       PGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRR-
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APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
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2005-02-11
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Pred. No.
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ing Prior Application data removed
OF SEQ ID NOS: 1158
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R APPLICATION NUMBER: 60/141,031

R FILING DATE: 1999-06-25

R APPLICATION NUMBER: 60/142,101

R FILING DATE: 1999-07-02

R APPLICATION NUMBER: 60/148,613

R FILING DATE: 1999-08-12
                                                                                                                                                                                                                                                                                                               Sequence 1146, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
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US-11-055-822-1146
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R FILING DATE: 1999-07-08
R APPLICATION NUMBER: DE 19
R FILING DATE: 1999-07-08
R APPLICATION NUMBER: DE 19
R FILING DATE: 1999-07-08
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larity 20.9%;
Conservative 55
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CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2005-02-
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 1
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 -EGLEKAEKIGYPVM-
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 -MSDQGFLTVSDDVYQQACIHTAE-
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
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larity 23.5%;
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PatentIn version
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                           EGGGGKG
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                           -IKETMMSDQGFLTVSD-----DVYQQACIHTAEEGLEKAEKIGYPVMIKAS
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Pred. No. 5
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CURRENT APPLICATION NUMBER: US/11/166,609
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: 10/412,000
PRIOR FILING DATE: 2003-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANT: TRIMNELL, MARY
OF INVENTION: NUCLEOTIDE SEQUENCES
OF INVENTION: METHOD OF USING SAMI
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larity 19.7%;
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PRIOR FILING DATE: 2000-03
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GENERAL INFORMATION:
APPLICANT: Ye, Rick W.
APPLICANT: Ye, Rick W.
APPLICANT: Miller, Edward S.
TITLE OF INVENTION: PROCESS FOR EXPRESSION OF FOREIGN GENES IN METHANE METABOLIZING TITLE OF INVENTION: BACTERIA THROUGH CHROMOSOMAL INTEGRATION
FILE REFERENCE: CL-2443 US NA
CURRENT APPLICATION NUMBER: US/11/070,080
CURRENT FILING DATE: 2005-03-02
PRIOR APPLICATION NUMBER: US 60/550385
PRIOR FILING DATE: 2004-03-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.3
SEQ ID NO 16
LENGTH: 423
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3.3%; Score 95; DB 7; Le
Best Local Similarity 21.1%; Pred. No. 4.2;
Matches 66; Conservative 57; Mismatches 124;
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5.1.7 Biocceleration Ltd version - 2006 GenCore (c) 1993 Copyright

model 38 using protein search, OM protein

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dates/sec ; Search time 203 Sec (without alignments) 1209.915 Million cell

PPPDHKAVSQFIGGNPLETA.... US-10-633-835-2 2907 1 PPPDHKAVSQFIGG Title: Perfect score: Sequence:

559

...LDGLIQDRLTAERPPADLAV

residues 2443163 segs, 439378781 0.5 Gapext BLOSUM62 Gapop 10.0 , Scoring table Searched:

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summaries

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ALIGNMENTS

SEQ ID NO:2. 559 AA ADJ47651 standard; protein; domain (first entry) maydis ACCase BC COA Acetyl 06-MAY-2004 ADJ47651; ACCase; RESULT 1 ADJ47651

carboxylase; carboxy transferase domain; domain; BC domain; fungicide. biotin carboxylase Ustilago maydis.

WO2004013159-A2. 12-FEB-2004. 04-AUG-2003; 2003WO-US024356

2002US-0401170P. 05-AUG-2002;

(CROP-) CROPSOLUTION INC.

Weatherly SC; SL, Volrath Elich TD,

WPI; 2004-180421/17

Novel peptide comprising acetyl CoA carboxylase (ACCase) having deleted biotin binding domain and carboxy transferase domain, and having functional biotin carboxylase domain, useful for identifying ACCase inhibitors/activators.

2; 56pp; English Claim 8; SEQ ID NO

The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxy transferase domain, and having a functional biotin carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in

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an assay to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity. A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be fungicide, employing the identified compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound that inhibits Acetyl CoA carboxylase activity. The present sequence represents an ACCase BC domain of the invention.
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Pred. No. 5.2e-261;
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1 Similarity 98.9%;
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Score 2222; DB 8; Pred. No. 1.4e-198; 49; Mismatches 83;

49;

2214 AA;

Sequence

Query Match

Length 2214;

63

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The present sequence is the protein sequence of the acetyl-CoA carboxylase (ACC) gene of Phaffia rhodozyma (ATCC 74438). The sequence shows 56.28% amino acid sequence identity to a known ACC from Emericella nidulans. ACC is an enzyme involved in fatty acid biosynthesis. Its substrate is acetyl-CoA, which is also involved in the carotenogenic pathway of P. rhodozyma. A claimed method for producing ACC comprises culturing a recombinant organism containing a vector comprising an ACC polynucleotide. Also claimed is a recombinant organism in which gene expression of ACC is reduced as a result of antisense technology, site-directed mutagenesis, error-prone PCR or chemical mutagenesis. The cerombinant organism is preferably P. rhodozyma or Xanthophylomyces dendrorhous containing a vector comprising an antisense polynucleotide. It is used in a claimed process for producing carotenoids such as astaxanthin, beta-carotene, lycopene, zeaxanthin and canthaxanthin. The method is useful for increasing microbial production of carotenoids such as a sataxanthin, which has antioxidant properties and is used as a colouring agent especially of farmed fish.
                                                                                                                                                                                                                                                                                                          New acetyl-CoA carboxylase polynucleotide derived from Phaffia rhodozyma or Xanthophylomyces dendrorhous, useful for producing a recombinant vector or for increasing microbial production of carotenoids.
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                                                                                                                                   2002EP-00021625
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N-PSDB; ADN10914, A
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                 WO2004029232-A2
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                                           . coenzyme A carboxylase; ACoACase; powdery mildew; fungus; acid biosynthesis; EC 6.4.1.2.
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RKPOPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGAL
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                                        FGHIFAYGADRSEARKQMVISLKELSIRGDFRTTVEYLIKLL
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2.7e-193;
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TGVDQVEVNDEGIVTVDKEVYMKGCVQSWQEGLEKAREIGFPVMIKASEGGGGKGIRKVD
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biotin binding domain and carboxy transferase domain, and having
functional biotin carboxylase domain, useful for identifying ACCa
inhibitors/activators.
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                                                                                                                                                                                                                                                                                                                     protein;
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biotin carboxylase
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86

KWAYET

HKAVSOFIGGNPLETAPASPVADFIRKOGGHSVITKVLICNNGIAAVKEIRSIR

61;

Matches

FGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAE

65

8

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Gaps

; 0

Indels

RAGVHA

carbohydrate;

kecombinant DNA construct; transformed plant; improved plant I cold tolerance; heat tolerance; drought tolerance; herbicide; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbc nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

#3698

polypeptide

entry)

(first

02-DEC-2004

ADN21045;

property;

4

Wed

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carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxy transferase domain, and having a functional biotin carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator.

The method further involves employing the identified binding compound in an assay to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity, A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, determining whether or not the compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound in inhibition of Acetyl CoA carboxylase activity, and selecting a compound to the inhibits Acetyl CoA carboxylase activity, The present sequence represents an Accase BC domain of the invention.
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                                  identifying
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larity 73.5%; Pred. No. 5.4e-194;
Conservative 59; Mismatches 88;
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to provide

New recombinant DNA construct comprising a promoter positioned to provier expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties

Goldman BS;

Chen X,

Slater SC,

Hinkle GJ,

Cao Y,

2004-061375/06

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GOLDMAN B

(GOLD/)

CHEN X

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CAO Y. HINKLE SLATER

(CAOY/)

(HINK/) (SLAT/) (CHEN/)

20-FEB-2003; 2003US-00369493

US2003233675-A1

Bacteria

18-DEC-2003

2002US-0360039P

21-FEB-2002;

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to prowide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to plant disease, better growth rate by modification of increased rate of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved lightin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form improved specification but was obtained in electronic forms from inspin of rendata mandom content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from USPTO at segdata.uspto.gov/seguence.html
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                      42;
2301;
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Length
Score 2139; DB 8;
Pred. No. 9.5e-191;
58; Mismatches 86;
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73.6%;
ilarity 68.8%;
Conservative 50
Query Match
Best Local Similarity
Matches 411; Conser
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2301

standard; protein;

ADN21045

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RESULT 5 ADN21045

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2003US-00369493

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CHEN X. GOLDMAN

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CAO Y. HINKLE SLATER

(CAOY/) (HINK/) (SLAT/) (CHEN/) (GOLD/)

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to prowide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant with the such as maize or soybean. The method of producing a transformed plant construct and growing the transformed plant where the polynucleotide or polypeptide is useful for improving plant with the recombinant DNA construct is useful for improving plant with the polynucleotide or polypeptide is useful for improving plants with the recombinant DNA construct is useful for improving plants with the plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth regulators, increased rate of the cell cycle pathway with plant growth regulators, increased rate of content, improved plant growth and development under at least one stress providing improved lightin production of improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained in electronic correct.
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                                                                                   New recombinant DNA construct comprising a promoter positioned to proview for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties
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                 Goldman
                                                                                                                                                   2130; 122pp; English
                Chen X,
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carboxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents acetyl CoA carboxylase (ACCase) isolated from Candida albicans. The C. albicans ACCase is used in an assay to identify inhibitors of the enzyme. This is useful in pharmaceutical research. Inhibitors of ACCase are useful as antifungal agents. The invention also provides a novel expression system using Saccharomyces cerevisiae to express the C. albicans ACCase gene in quantifiable amounts. Expression of the C. albicans ACCase gene in S. cerevisiae C overcomes prior art problems of isolation and purification of the ACCase. It is possible to achieve about 14-fold overexpression relative to the wild: type host S. cerevisiae strain JK9-3D. This is achieved by replacing the C. albicans promoter in the expression construct by a stronger and preferably inducible promoter such as the S. cerevisiae GALI promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
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                                                                                                                                                                                                                                                                                                                                                                                                                                A polynucleotide encoding an Acetyl-CoA carboxylase gene from Candida albicans overexpressed in Saccharomyces cerevisiae for purification and
        YETFGDE
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N-PSDB; AAX88525.
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ETMMSDQ-GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGE
                                                                                                                                                                                   TTEMVSGVNIPAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQ
                                                                                    EFKOLYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAIŞI FGRDÇSVQRRHQKI I
                                                                                                                             EAPVIIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHP
                                                                                                                                         delet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxy transferase domain, and having a functional biotin carboxylase domain. A peptide of the invention is useful for identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel peptide comprising acetyl CoA carboxylase (ACCase) having delebiotin binding domain and carboxy transferase domain, and having functional biotin carboxylase domain, useful for identifying ACCase inhibitors/activators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxylase; carboxy transferase domain; BC domain; fungicide.
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20-JUN-2003

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the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator.

The method further involves employing the identified binding compound in a sasy to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity. A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, the presence of binding indicating the compound is or may be fungicide, employing the identified compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound the inhibits an ACCase BC domain of the invention.
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Sequence 580 AA;

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                                                                 Length 580;
                Indels
                99;
Score 2060; DB 8;
Pred. No. 2.6e-184;
5; Mismatches 89
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70.9%;
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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 HAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.9%; Score 2060; DB 6;
larity 69.1%; Pred. No. 2.1e-183;
Conservative 76; Mismatches 89;
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Superti-Purga GD;
                                                drug
                                                eukaryote;
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                       ID 325
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                                                                       cerevisiae
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                       Protein sequence #SEQ
                                               complex;
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M, Schultz
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                                                                      Saccharomyces
                                              Multiprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament of for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was
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       KTORKPOPOGHVVACRITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYA
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drug screening, or in diagnosing or screening for the presence
disease or disorder, or a predisposition for developing a disea
disorder in a subject.
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10 A, Bauch
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Kruse U,
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P, Krause R,
C, Rick J;
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M, Grandi
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Marzioch M, Granu.
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N-PSDB; ADK61969.
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dyslipidaemia
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                                        DB 7;
1.1e-183;
1es 89;
                                           ore 2060; Ded. No. 2.1e
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                                                                                                                                        obesity
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                                                                                                                                                                                          carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-CoA) carboxyltransferase (CT) domain of the invention is useful for treating: metabolic syndrome, diabetes, obesity, cardiovascular disease, atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia, hypertension, hyperuricaemia and renal disfunction. The present amino acid sequence represents a yeast acetyl-CoA carboxylase of the invent:
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                                                                                                                           composition comprising a carbox (COA) carboxylase, for treating ease, atherosclerosis, or cancer
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ed. No. 2.5e-183;
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       2003US-0439383P.
2003US-0459464P.
2003US-0491640P.
2003US-0514636P.
2004US-00514636.
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to prowide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant such as maize or soybean. The method of producing a transformed plant such as maize or soybean. The method of producing a transformed plant such as maize or soybean. The method of producing a plant with the recombinant DNA construct and growing the transforming plant with the polynucleotide or polypeptide is useful for improving plant with the comproved plant properties, e.g. improved cold, heat or drought tolerance. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress proved the condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial nolvmential.
                                                                                                                                                        property;
                                                                                                                                                                                                                        carbohydrate;
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ince; herbicide;
                                                                                                                                                                                        resistance;
                                                                                                                                                             cold tolerance; heat tolerance; drought tolerance; herbicide pathogen tolerance; pest tolerance; plant disease resistance cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carl nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
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                 standard; protein;
                                                                                                                   Bacterial polypeptide #1998
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DDLITHKMTAEKPDPTLAV

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scope of

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oction. This sequence represents a bacterial polypeptide used in the of the invention. Note: The sequence data for this patent did not part of the printed specification but was obtained in electronic t from USPTO at sequence.html.

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|SVRKWAY
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                                          --FIGLNTVDKLEESPLRDFVKSHGGHTVISKILIANNGIAAVKEIR
                                                                    ETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNYANVDLIVD
                                                                              SGTGIKETMMSDQ--GFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASE
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    Pred. No. 2.5e-18. / Mismatches 8
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to prowide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress conduction, improved plant growth and development under at least one stress conduction. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic conduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337
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                                                                                                                                A construct comprising a promoter positioned to prova
a polynucleotide encoding a polypeptide from a
useful for producing plants with improved properties
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Pred. No. 7.3e-168;
; Mismatches 94;
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Local Similarity 64.3%;
les 355; Conservative (
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        FKTORKPOPOGHVVACRITAENPDIGFKPGMGALIELNFRSSISTWGYFSVGTS
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                                                                                                                                                                                                                                                                                       Bauch A
                                                                                                                                                                                                                                                                               Schultz J;
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Merino A,
                                                                                                                                                        Disease treating protein complex-derived protein #1382
                                                                                                                                                                                                                                                                               Kuester
                                                                                                                                                                                                                                                                              Superti-Furga G, Kueste
P, Krause R, Kruse U,
C, Rick J;
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                                                                                                                                                                        drug target; diagnosis.
                                                                                                             standard; protein; 2000 AA
                                                                                                                                                                                                                                  20-DEC-2002; 2002EP-00102902
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Marzioch M, Grandi P
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N-PSDB; ADK63987.
                                                                                                                                                                        protein complex;
                                                                                                                                                                                      Unidentified
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The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for the print of the print spatent did not form part of the print of protein but was electronic format). EPO in the this patent obtained fr

Sequence 2000 AA;

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239
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                                                       ---QFIGLNTVESAQPSILRDFVDLRGGHTVISKILIANNGIAAVKEMRSIRKWA
                                                                                   ORRHOKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELN
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                                                                                                                                                                                                                                            2000;
             17;
               Indels
5; DB 7;
.4e-167;
es 94;
                                                                                                                                                                                                                                                                                                                                                                                                       carboxylase; carboxy transferedomain; BC domain; fungicide;
Score 1889.5;
Pred. No. 2.4e
6; Mismatches
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larity 64.3%;
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      1 Similarity 355; Conser
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biotin carboxylase
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                                                                                                                                                                                                                                                                                                                                                                                         Human ACC1 BC
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The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be ested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in an assay to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity. A peptide of the invention is also useful for identifying fungicides, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, determining whether or not the compound in an assay to detect may be fungicide, employing the identified compound in an assay to detect
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Novel peptide comprising acetyl CoA carboxylase (ACCase) having biotin binding domain and carboxy transferase domain, and havin functional biotin carboxylase domain, useful for identifying AC
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                                                                     English
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                                                                     26pp;
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ilarity 63.8%;
Conservative 75
                                                                     SEQ ID NO 10;
                                         inhibitors/activators
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may be fungicide, e
inhibition of Acety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises a crystallisable composition containing a carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-CoA) carboxylase. The composition of the invention is useful for treating metabolic syndrome, diabetes, obesity, cardiovascular disease, atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia, hypertension, hyperuricaemia and renal disfunction. The present aming acid sequence represents a human acetyl-CoA carboxylase of the invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                          acetyl-coenzyme A carboxylase; acetyl-CoA carboxylase;
metabolic syndrome; diabetes; obesity; cardiovascular disease;
atherosclerosis; depression; cancer; hyperlipidaemia; dyslipidaemia;
hypertension; hyperuricaemia; renal disfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osition comprising a carboxyltransferase carboxylase, for treating e.g. diabetes, atherosclerosis, or cancer.
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larity 63.6%; Pred. No. 1.4e-157;
Conservative 79; Mismatches 104;
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                                                                                                                                                                                                                                              enzyme; ACC1
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                                                                                                                                                          Human acetyl-coenzyme A carboxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crystallizable composition yl-coenzyme A (CoA) carboxy
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2003US-0459464P.
2003US-0491640P.
2003US-0514636P.
2004US-00514636.
                                                                                                                                                                                                                                                                                                                                              2004WO-US000585
                                                                                                                                                                                                                                              crystallisable composition;
                                                                                 ADQ90744 standard; protein;
                                                                                                                                                                                  carboxyltransferase
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nes 344; Conser
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31-MAR-2003;
31-JUL-2003;
27-OCT-2003;
09-JAN-2004;
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              complex of BRCAl protein and acetyl coenzyme A-car in screening agents suitable for treatment, preven cancer.
LL - - KNGIAFMGPPSQAMWALGDKIASSIVAQTAGIPTLPWSGSGLRVDWQEND
                                              EVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPV
                                                       499 KOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAER
                                                                                                               AAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGHV
                                                                                                                                --HVPCPRGHV
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                                                                                                                                                                                                                                                                                                                      coenzyme A-carboxylase
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                                                                                                                      Lenoir G,
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5-MAR-2002; 2002FR-00002789
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N-PSDB; ABZ23503.
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diagnosis of
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The present sequence represents human acetyl coenzyme A-carboxylase alpha (ACC-alpha). The ACC-alpha protein was used in the course of the invention. The specification describes a molecular complex comprising a polypeptide having amino acids 1640-1663 of the human BRCA1 protein (or

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similar sequence from some other animal species), and a polypeptide that is a part of the acetyl coenzyme A-carboxylase alpha (ACC-alpha) protein able to bind the BRCAl protein. The complex is implicated in predisposition to cancer of breast and ovary. It is used to screen for compounds that modulate interaction between BRCAl and ACC-alpha, which are potentially useful for treatment, prevention and diagnosis of cancer, and to identify endogenous ligands. Modulated formation of the complex can be used for diagnosis of cancer. Antibodies directed against specific parts of human ACC-alpha are useful for localization of the complex in
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-HVPCPRGHVIAARIT
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                                                                                                                                                 2346
                                                                                                                                                                       Indels
                                                                                                                                                 Length
                                                                                                                                               Score 1781; DB 6;
Pred. No. 5.2e-157;
); Mismatches. 104;
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ilarity 63.6%;
Conservative 7
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                                                                                                                                                                                                                                          acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer;
              ASPVADFIRKOGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
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he present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPV
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Pred. No. 5.2e-157
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larity 63.6%;
Conservative 73
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2002FR-00002788
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              Misc-difference
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05-MAR-2002;
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The present sequence is a variant sequence for human acetyl-Coenzyme A carboxylase-alpha (ACC-alpha). This sequence can be used for in vitro

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diagnosis of cancer (or of an increased risk of developing it), by detecting ACC-alpha gene mutations or polymorphisms, or altered ACC-alpha protein expression, relative to a control population. The method is particularly used to diagnose cancer, especially of breast or ovary, or for assessing the risk of developing such cancers. Note: The present sequence was not shown in the specification, but was derived from
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Pred. No. 5.2e-157;
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-NPPNKPRPSGHVIAARITSENPDEGF
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                                                                                              carboxylase,
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                                                                                                                                                                                                                                                                       carboxylase;
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Pred. No. 6.5e-157;
9; Mismatches 110;
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                                                                                                                                                                                                                                                                   Acetyl-
enzyme.
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                                                                                                                                                                                                                                           Drosophila melanogaster ACCase SEQ ID NO
|||||| ::||| ||| || || GIPLYRLKDIRLLYGESPWGSSVIDFE
                                                                                                                                                                                                                                                                   Drosophila melanogaster; fruit fly; insecticide; acaricide; EC 6.4.1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding insect for identifying insecticidal and and modulators.
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                                                                                           VMKLAGQARHLEVQLLADQYGNAISIPGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKA
                                                                                                                                             HKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSDQGFLTVSDDVYQ
        EGGGGKGIRKCTNGEEFKOLYNAVLGEVPGSPVF
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                                                                                                                                                                                                                                                                                                               New nucleic acid encoding bovine acetyl coenzyme A carboxylase its promoter, for milk-specific production of proteins and for fat content of milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               carboxylase-alpha protein fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -coenzyme A carboxylase-alpha; acetyl-coA; milk gland-specific promoter; Accalpha; fat content; genotyping; lactation.
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(by cattle, sheep or goats) has reduced fat content. Analysis of the polymorphic 933-966 region of (Accalpha) is useful for genotyping animals, producing a genotype that is directly correlated with Accalpha expression during lactation and with fat content of the milk. This makes it possible to generate populations of cattle that produce milk of high or low fat content by classical breeding methods. Accalpha is a lactation-specific, inducible promoter for expressing foreign proteins in the milk and, when modified, results in milk of reduced fat content, which facilitates recovery of proteins. This sequence represents a fragment from bovine Accalpha which contains a fragment of exon 5A exon 6 and exon?
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biotincarboxylase; carboxyl-transferase;
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1 Similarity 63.0%; Pr
341; Conservative 83;
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                                                                                                                                        Disclosure; Fig 2; 14pp;
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N-PSDB; AAQ04013.
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorder, endocrine autoimmune/inflammatory disorders, developmental disorders, or disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lew diagnostic and therapeutic polynucleotides and polypeptides in diagnosing a condition, disease or disorder associated with olecules, e.g. autoimmune or inflammatory disorders, in gene t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; human diagnostic and therapeutic polynucleotide;
                                                                                                                                                                                                                                                                                                                                                        Wright RJ, Bruns CM, Marjanovic MM, Shen F;
TA, Suchorolski MT, Altus CM, Pitts SJ, Elder I
Delegeane AM, Panesar IS, Banville SC, Reddy TP,
Blanchard JL, Panzer SR, Wang X, Au AP, Gerst
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LI
Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirt
G M, Policky JL, Hurwitz BL, Ma Y, Jackson JL,
Shi X, Suarez CJ;
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                                                                             Human diagnostic and therapeutic pprotein SEQ
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                                                                                                                                                                                                                                                                        12-SEP-2002; 2002US-0410259P
12-SEP-2002; 2002US-0410260P
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                                                   entry)
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N-PSDB; ACN42221.
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in gene mapping
                                                                                                                                             Homo sapiens.
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                                              18-NOV-2004
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Peralta CH,
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                                    LTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL
AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; drug metabolising enzyme; anti-HIV; antiallergic; antilipaemic; antidiarrhe antiniflammatory; antianaemic; thrombolytic; antilipaemic; antityroid; antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid; cytostatic; hepatotropic; virucide; dermatological; antidiabetic; nephrotropic; antigout; neuroprotective; thyromimetic; osteopathic; antiarthritic; antipsoriatic; uropathic; ophthalmological; antirheumathaemostatic; gene therapy; cell proliferative disorder; cancer; developmental disorder; endocrine disorder; eye disorder; metabolic disorder; jaflammatory disorder; liver disorder; autoimmune disorder; inflammatory disorder; DME-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEO ID
                                                                                                                                                                                                     Human drug metabolising enzyme, DME-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                standard; protein; 2458 AA
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2001US-0305402P.
2001US-0308158P.
2001US-0322127P.
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S, Swarnakar A,
Y, Gorvad AB, B
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13-JUL-2001;
27-JUL-2001;
14-SEP-2001;
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                                      198
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The present invention relates to novel human drug metabolising enzymes, DME-1 to DME-13 (ABP59210-ABP59222) and their coding sequences (ABZ81301-ABZ81313). The sequences are useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), endocrine (e.g. renal tubular acidosis, diabetes), eye disorders (e.g. glaucoma, keratitis), metabolic (e.g. hyperlipidaemia, cystic fibrosis), gastrointestinal disorders (e.g. pastroenteritis, diarrhoea), liver disorders (e.g. hepatitis, Reye's syndrome), or autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma, autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma, autoimmune thyroiditis, irritable bowel syndrome, rheumatoid arthritis, solderatitis, Reiter's syndrome, rheumatoid arthritis, syndrome, uveitis). They are also useful in the assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of DME. The polynucleotides encoding DME are useful
                                                                         New drug metabolizing enzymes (DME) useful for diagnosing, treating preventing diseases or conditions associated with aberrant DME expression, e.g. cancer, AIDS, atherosclerosis, diabetes, glaucoma, hepatitis or osteoporosis.
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  WPI; 2003-221588/21
                          N-PSDB; ABZ81302
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2458 AA; Seguence

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7; 363 197 421 257 317 900 436 652 496 712 556 141 481 81 ||:||| NPKLPEL 22 ASPVADFIRKOGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES LTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGGGGIRKCTNGEEFKQLYNAVL PVTIAPE PATIAPL AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKT-QRKPQPQGHVVACR **ARKQMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPAD** ITAENPOTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSOFGHIFAYGADRSE WGENREE MVSGVNI Gaps DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTE 17; Length 2458 Indels Score 1769.5; DB 6; Pred. No. 6.8e-156; 5; Mismatches 107; 75; Match 60.9%; Local Similarity 63.4%; nes 344; Conservative 75 83 245 304 142 542 Query Match 198 422 258 482 318 378 497 713 364 601 437 653 Best Loc Matches D D d D ದ್ದ a a Q Q g ò g 8 ò ઠ ठ ઠ ઠે ઠે 8

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This invention describes novel secreted proteins (SECP) which have antiarteriosclerotic, antiatherosclerotic, hepatotropic, cytostatic, antiarteriosclerotic, antianaemic, antidiabetic, antiallergic, antiarthratic, antiulcer, antipsoriatic, vasotropic, antiinflammatory, neuroprotective, antiulcer, antipsoriatic, vasotropic, antirheumatic, antiarthritic, cardiant, hypotensive, anticonvulsant, nootropic, immunosuppressive, antiparkinsonian and ophthalmological activity. The polynucleotides and polypeptides of the invention can be used for diagnosing, treating or preventing cell proliferative disorder e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, cancer, autoimmune/inflammatory disorders e.g. acquired immunodeficiency syndrome
                                                                                                                                                                                                                                    Secreted protein; SECP; human; antiarteriosclerotic; antiatherosclerotic; hepatotropic; cytostatic; anti-HIV; antiallergic; antiathmatic; cancer; antianaemic; antidiabetic; antiinflammatory; neuroprotective; antiulcer; antiarthritic; cardiant; hypotensive; gonadal dysgenesis; vasotropic; anticonvulsant; nootropic; immunosuppressive; pericarditis; antiparkinsonian; ophthalmological; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; angina pectoris; autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy; ulcerative colitis; cardiovascular disorder; myocardial infarction; Raynaud's disease; myocarditis; neurological disorder; cataract; Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease; developmental disorder; Duchenne muscular dystrophy; antipsoriatic;
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Ison CH;
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Griffin JA, He A, Honchell CD,
Lu DAM, Mason PM, Sanjanwala I,
Tang YT, Thangavelu K, Tran
                                                                                                                                                                                                        protein from clone 7757335CD1 SEQ ID
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s. psoriasis, asthma,
Alzheimer's disease.
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Tang YT,
, Yue H;
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                                                                                                             2487 AA
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2001US-0282112P.
2001US-0282702P.
2001US-0383855P.
2001US-0343718P.
2001US-0339236P.
2002US-0357002P.
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                                                                                                             standard; protein;
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Xu Y,
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Gietzen KJ,
Lee S,
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N-PSDB; ABS57545.
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06-APR-2001;
09-APR-2001;
13-APR-2001;
19-OCT-2001;
07-DEC-2001;
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Swarnakar A,
                                                                                                                                                                           11-FEB-2003
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cardiovascular disorder e.g. myocardial infarction, angina pectoris, etc; cardiovascular disorder e.g. myocardial infarction, angina pectoris, etc; cardiovascular disorder e.g. myocarditis, pericarditis, etc; cardiovascular disorders e.g. epilepsy, Huntington's disease, Parkinson's disease, Alzheimer's disease, Creutzfeldt-Jakob disease, Parkinson's disease, Alzheimer's disease, Creutzfeldt-Jakob disease, etc; and disorders e.g. Duchenne and Becker muscular dystrophy, cataract, gonadal dysgenesis, Cushing's syndrome, etc. The products of the invention can also be used for drug screening, proteome analysis, microarrays creating knock-in humanised animals or transgenic animals to microarrays creating knock-in humanised animals or transgenic animals to transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences. ABB84649-ABB84673

represent secreted proteins encoded by the cDNA's shown in ABS57545-
ABS57569, described in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                  Score 1769.5; DB 6
Pred. No. 6.9e-156;
5; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.4%; Pre
Matches 344; Conservative 75;
                                                                                                                                                                                                                                                                                                                                Sequence 2487 AA;
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2498 AA

standard; protein;

ABU65149

GH

(first entry)

20-MAY-2003

ABU65149;

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antiarteriosclerotic; antiasthmatic; cancer; bronchial asthma; gene therapy; vaccine;
                                                                                                                                                                          2001US-0274194P.
2001US-0274281P.
2001US-0274332P.
2001US-0274849P.
2001US-0275235P.
2001US-0275235P.
2001US-0275235P.
2001US-0275239P.
2001US-0275239P.
2001US-0277321P.
2001US-0277321P.
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2001US-0277321P.
2001US-0277321P.
2001US-0277321P.
2001US-0277321P.
2001US-0277321P.
2001US-0277338P.
2001US-0277338P.
2001US-0277338P.
2001US-027733P.
2001US-0288944P.
2001US-027733P.
2001US-027733P.
2001US-027733P.
2001US-0288944P.
2001US-027733P.
2001US-027733P.
2001US-0298342P.
2001US-0288966P.
2001US-028899P.
2001US-0291240P.
2001US-0294485P.
2001US-0294485P.
2001US-0294485P.
2001US-0294485P.
2001US-0294485P.
2001US-0294485P.
2001US-0294303P.
2001US-0393380P.
2001US-0393380P.
2001US-0333380P.
2001US-03323112P.
2001US-03323112P.
2001US-03322711P.
                     NOVX; cytostatic; cardiant; hypotensive; cardiomyopathy human.
                                                                                                  WO200272757-A2
                                                                                                                                                     08-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2001;
16-AUG-2001;
10-SEP-2001;
12-SEP-2001;
27-SEP-2001;
                                                                                                                                                                            08-MAR-2001;
08-MAR-2001;
08-MAR-2001;
09-MAR-2001;
12-MAR-2001;
13-MAR-2001;
13-MAR-2001;
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16-MAR-2001;
19-MAR-2001;
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27-MAR-2001;
28-MAR-2001;
30-MAR-2001;
30-MAR-2001;
02-APR-2001;
02-APR-2001;
04-APR-2001;
04-APR-2001;
03-MAY-2001;
03-MAY-2001;
15-MAY-2001;
16-MAY-2001;
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23-MAR-2001;
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31-MAY-2001;
31-MAY-2001;
18-JUN-2001;
19-JUN-2001;
10-JUL-2001;
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Human
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(first
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08-MAR-2001;

08-MAR-2001;

09-MAR-2001;

13-MAR-2001;

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13-MAR-2001;

14-MAR-2001;

20-MAR-2001;

20-MAR-2001;

20-MAR-2001;

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20-MAR-2001;

21-MAR-2001;

22-MAR-2001;

23-MAR-2001;

24-MAR-2001;

25-MAR-2001;

27-MAR-2001;

27-MAR-2001;

28-MAR-2001;

29-MAR-2001;

30-MAR-2001;

                                            160
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                                                                                                                            01-JUL-2004
                                                                                                          ADN61949;
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                                                                                                                                                                                                                                                 enting or
or activity
bronchial
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QP.
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                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                      polynucleotides, useful for preventing or treating with aberrant NOVX expression or activity e.g., atherosclerosis, cardiomyopathy or bronchial
                                                                                         Anderson
sobrook J
                                                                                                                                                                                                                         cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotens activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activie. G. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchia asthma. The products of the invention can be used for gene therapy or a vaccine. ABU65041-ABU65218 represent the NOVX polypeptides encoded b ABX97008-ABX97185
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GHVIAAR
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요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEA
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Pred. No. 7e-156;
75; Mismatches 107;
                                                                   Ji W, Gorman, i E, Vernet CAM, (SJ, Malyankar UM,
                                                                     Gorman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 313-314; 1103pp; English
                                                              Shenoy
                                                                                                                                                                                                                                                                                                                                                   75;
                                                                                                                                                                                                                      invention describes novel
2001US-0338092P.
2001US-0337185P.
2002US-0345705P.
2002US-00092900.
                                                                                                                                                                                                                                                                                                                                 Match 60.9%;
Local Similarity 63.4%;
les 344; Conservative 7
                                                                      Gusev V, Ji
Gangolli E,
Casman SJ,
Catterton E,
                                                              Spytek KA,
                                                                                                          Rieger DK;
                                                                                                                                                      NOVX polypeptides and
a disorder associated
cancer, hypertension,
                                             CURAGEN CORP
                                                                                                                           WPI; 2002-723332/78
N-PSDB; ABX97116.
                                                                                                                                                                                                                                                                                                                 2498 AA;
                                                             Padigaru M, S
Zerhusen BD,
Patturajan M,
03-DEC-2001;
04-DEC-2001;
03-JAN-2002;
07-MAR-2002;
                                                                                        Fernandes ER,
Spaderna SK,
                                                                                                           Lepley DM,
                                                                                                                                                                                                   Claim 1;
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                                                                                                                                                                                                                                                                                                                 Sequence
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us-10

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New NOVX polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. cancer, diabetes infection or obesity, and in chromosome mapping, tissue typing or
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Ji W, Gorman L, Miller CE, Kekuda R;
EA, Vernet CAM, Guo XS, Tchernev VT;
, Malyankar UM, Gerlach V, Liu Y;
K, Catterton E, Leite MW, Zhong H;
, Rieger DK, Burgess CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218; 786pp; English
2001US-0299310P.
2001US-0304354P.
2001US-0318462P.
2001US-0318462P.
2001US-0318770P.
2001US-0325430P.
2001US-0325681P.
2001US-0325681P.
2001US-0332572P.
2001US-0332272P.
2001US-0332272P.
2001US-0332272P.
2001US-0332272P.
2001US-0332272P.
2001US-033272P.
2001US-0332094P.
2001US-0337426P.
2001US-0337426P.
2001US-0337485P.
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Spaderna SK,
Lepley DM, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EA,
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Gusev VY,
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GANGOLLI E A.
VERNET C A M.
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FERNANDES E R
CASMAN S J.
MALYANKAR U M
GERLACH V.
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                                                                                                                                                                             PADIGARU M.
SPYTEK K A.
SHENOY S G.
TAUPIER R J.
PENA C E A.
LI L.
ZERHÜSEN B D
                                                                                                                                                                                                                                                                                                                                                                                                                      LEPLEY D M.
RIEGER D K.
BURGESS C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-225693/21
N-PSDB; ADN61948.
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X
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JI W.
GORMAN L.
MILLER C E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing or tree infection or obesipharmacogenomics.
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19-JUN-2001;
31-JUL-2001;
16-AUG-2001;
10-SEP-2001;
12-SEP-2001;
27-SEP-2001;
27-SEP-2001;
18-OCT-2001;
14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
14-NOV-2001;
03-DEC-2001;
03-DEC-2001;
03-DEC-2001;
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Patturajan M,
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Anderson DW,
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(LIUY/
(ANDE/
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included are an isolated nucleic acid molecule encoding NOVx, a vector comprising the nucleic acid, a cell comprising the vector, methods for determining the presence or amount of the polypeptide or the nucleic acid molecule in a sample, methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject, a method for identifying an agent that binds to the above polypeptide, a method for identifying a potential therapeutic agent for use in the treatment of a pathology that is related to aberrant expression or physiological interactions of the polypeptide, a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide and a method for modulating the activity of the polypeptide cited above. The composition and methods are useful for diagnosing, preventing or treating diseases such as disease, ineurodegenerative disorders like Alzheimer's disease or dyslipidaemias, and other chronic diseases. These may also be used in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The polypeptides are also useful as vaccines. The present sequence represents a NOVX protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKT-ORKPOPQGHVVACR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARKOMVISLKELSIRGDFRITVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPAD
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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3
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Pred. No. 1.2e-154;
5; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                               60.4%;
llarity 63.0%;
Conservative 7
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Best Local Similarity
Matches 342; Conser
                                                                                                                                                                                                                                                                                                                                   Sequence 2498 AA;
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774 AA

ADJ47656 standard; protein;

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RESULT 31
ADJ47656
ID ADJ4

or amino

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The invention relates to an isolated polypeptide (designated NOVX, NOV1-NOV127) comprising a sequence selected from 178 fully defined acid sequences (and their mature forms, variants and fragments). A

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The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                     497 ARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAERPPAD
              LTVSDDVYQQACIHTABEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAVL
                                                                                                                      DARESMEKAAVRLAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLQVEHPTTEMVSGVNI
                                                                                                                                     AIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVNL
                                                                                                                                                                           PAAQLQVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKT-QRKPQPQGHVVACR
                                                                                                                                                                                                                                 ITAENPDTGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSE
                                                                                                                                                                                                                                              for preparing a r treating psoriasis
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pharmaceutical composition for diagnosing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schoenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 28; 3069pp; English.
                                                                                                                                                                                           ADN03634 standard; protein; 2206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antipsoriatic protein sequence #14.
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N-PSDB; ADN03633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2206 AA;
                                                                                                                                                                                                                                                                                                                                                 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical
                                                                                                                                                                                                                                                                                                                                               LAV
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                                                                                                                                                                                                                                                                                                                                                                           LGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-2004
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                                                                                                                                                                                                                                                                                                               713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN03634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxylase (ACCase) having a deleted biotin binding domain, having a carboxylase (ACCase) having a functional biotin carboxylase domain. A peptide of the invention is useful for identifying ACCETYL COA carboxylase inhibitors or activators, which involves combining the peptide and a compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in an assay to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity, and selecting a compound that inhibits or biotin carboxylase compound to be tested for the ability to bind to the biotin carboxylase domain, the presence of binding to the biotin carboxylase compound to be tested for the ability to bind to the biotin carboxylase domain, the presence of binding indicating the compound is or may be fungicide, employing the identified compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound to that inhibits Acetyl CoA carboxylase activity, The present sequence that inhibits Acetyl CoA carboxylase activity. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pound is or
y to detect
compound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASPVADFIRKOGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFTVMATPED
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                                                                                                                                                                                                                                                                                                                                                                 ng
Case
                                                                                                                                                                                                                                                                                                                                                 Novel peptide comprising acetyl CoA carboxylase (ACCase) having
biotin binding domain and carboxy transferase domain, and havin
functional biotin carboxylase domain, useful for identifying AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 774;
                                                                             carboxylase; carboxy transferase domain; domain; BC domain; fungicide; human; ACC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.8%; Score 1738; DB 8; 62.8%; Pred. No. 9.1e-154; ive 76; Mismatches 108;
                                                                                                                                                                                                                                                                                            SC;
                                                                                                                                                                                                                                                                                                                                                                                                                   56pp; English
                                                                                                                                                                                                                                                                                         Weatherly
                                                     Human ACC2 BC domain SEQ ID NO:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                         2003WO-US024356
                                                                                                                                                                                                                                    2002US-0401170P
                         entry)
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                                                                                                                                                                                                                                                                                         Volrath SL,
                                                                                                                                                                                                                                                                                                                                                                                          inhibitors/activators.
                                                                                                                                                                                                                                                               CROPSOLUTION
                          (first
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                                                                               COA
                                                                                            biotin carboxylase
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                                                                                                                                                  WO2004013159-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 774 AA;
                                                                              ACCase, Acetyl
                                                                                                                                                                                                                                 05-AUG-2002;
                                                                                                                                                                                                        04-AUG-2003;
                                                                                                                      Homo sapiens
                          06-MAY-2004
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Best Local
Matches 34
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|LETESF
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                   Gaps
                                 ANVDL
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                                                                                                                                                                                                                                                                                                                                                                                                                     disease;
dyslipidae
                                IRSIRKWAYETFGDERAIEFTVMATPEDLKVNADYIRMADQYVEVPGGSNNNNY
                                        VDVAERAGVHAVWAGWGHASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKIS
                                                                      SEGGGGKGIRKCTNGEEFKOLYNAVLGEVPGSPVFVMKLAGOARHLEVQLLAD
                                                                                                                                   SIFGRDCSVQRRHQKIIEEAPVTIAPEDARESMEKAAVRLAKLVGYVSAGTVEW
                                                                                                                                                                   DFDFSSPESFKTQRKPQPQGHVVACRITAENPDTGFKPGMGALTELNFRSSTST
                                                                                                                                                                                                                                                       SIRGDFRTTVEYLIKL
                                                                                                                                                                                                                                                             2206
                   13;
    Length
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                 acetyl-coenzyme A carboxylase; acetyl-CoA carboxylase; metabolic syndrome; diabetes; obesity; cardiovascular atherosclerosis; depression; cancer; hyperlipidaemia; hypertension; hyperuricaemia; renal disfunction; crystallisable composition; enzyme; ACC2
          .49;
98;
    Ø
    5; DB
                                                                                                                                                                                                                                                    GTSGALHEYADSQFGHIFAYGADRSEARKQMVISLKEL
  ore 1697.5;
ed. No. 3.4e
Mismatches
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   Score
Pred.
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                74;
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2003US-0459464P.
2003US-0491640P.
2003US-0514636P.
2004US-00514636.
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  protein;
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                                                                                                                                                                                                                                                                                                                                                                                       acetyl-coenzyme
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Query Match
Best Local Similarity
Matches 324; Conser
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31-MAR-2003;
31-JUL-2003;
27-OCT-2003;
09-JAN-2004;
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                                                                         domain of obesity,
                                                                                                                                                    The invention comprises a crystallisable composition containing a carboxyltransferase (CT) domain of acetyl-coenzyme A (acetyl-CoA) carboxylase. The composition of the invention is useful for treating: metabolic syndrome, diabetes, obesity, cardiovascular disease, atherosclerosis, depression, cancer, hyperlipidaemia, dyslipidaemia, hypertension, hyperuricaemia and renal disfunction. The present amino acid sequence represents a human acetyl-CoA carboxylase of the invention
                                                                                                                                                                                                                                                                                                                                          81
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                                                                         New crystallizable composition comprising a carboxyltransferase acetyl-coenzyme A (CoA) carboxylase, for treating e.g. diabetes cardiovascular disease, atherosclerosis, or cancer.
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Pred, No. 1.8e-146;
79; Mismatches 117;
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Best Local Similarity 60.8%;
Matches 330; Conservative 75
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                                                                                                                             SEQ ID NO
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                                                                                                                                                                                                                                                            Sequence 2483 AA;
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ADQ39507
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further comprises: an isolated nucleic acid molecule comprises; an isolated by the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a nucleic acid molecule; a method of detecting acidinal infarction. The novel detection method has cardiant activity.

The novel detection may be used in gene therapy. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method for identifying an individual has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one the nucleotide sequences given in the specification in the individual, nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The inventio further comprises: an isolated nucleic acid molecule comprising at lea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction associated gene containing one or more SNP's of the invention. Note:
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single nucleotide polymorp
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                                    infarction-associated gene derived protein,
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                                                                                        gene therapy; human.
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2003US-0453135P.
2003US-0466412P.
2003US-0504955P.
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   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying an individual myocardial infarction by d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; SEQ ID NO 1170;
                                                                       infarction;
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10-MAR-2003;
30-APR-2003;
23-SEP-2003;
                                                                                                                            Homo sapiens
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 18-NOV-2004
                                                                       Myocardial
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                                                                                                   LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASEN
          2483
                                 17;
          Length
                                 Indels
Score 1669.5; DB 8;
Pred. No. 1.8e-146;
          DB 8;
 57.4%; Sc.
60.8%; Pre
                                Conservative
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540 376 196 316 599 9 EDARESMEKAAVRIAKLVGYVSAGTVEWLYSPESGEFAFLELNPRLOVEHPTTEMVSGVN ITAENPDIGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYGADRSE LKANAEY I KMADHYGPAPGGPINNINYANVEL I VDI AKRI PLQAVWAGWGHALENPKLPEL **FLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYNAV** LAIFEFMEQCAIRLAKTVGYVSAGTVEYLYS-QDGSFHFLELNPRLQVEHPCTEMIADVN LAASKHKIIFIGPPG-SAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD 559 774 LAV 507 009 303 197 257 541 377 437 713 772 142 317 653 497 557 셤 d g a a d ð ð q ద ð ò ठे ò à

2483 4 standard; protein; SEQ ID entry) ι (first Human ACC2 protein 28-JUL-2005 AEA33628 **AEA336**

disease; atherosclerosis; heart 2004WO-AU001572 14-NOV-2003; 2003AU-00906285 14-NOV-2003; 2003AU-00906286 obesity; diabetes; WO2005047525-A1 15-NOV-2004; 26-MAY-2005 Ношо CCXSXBXBXBXBXBXBXBXBXBXBXBXBXBXBXCCC

ACC2

Molero-Navajas RES GARVAN INST MEDICAL Cooney GJ, 2005-386363/39 James D, (GARV-)

Identifying a modulator of whole body insulin sensitivity of an animal determining the AMP-dependent protein kinase or acetyl CoA carboxylase activity or free fatty acid level or oxidation in the animal administerwith a compound.

296pp; English Disclosure; SEQ ID NO

The invention comprises a method of identifying a compound that enhances or reduces whole body insulin sensitivity of an animal. The method

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protein
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involves administering a compound to a non-human animal, isolated tissue or cell having reduced expression of functional multi-adaptor protein Cbl, and determining the activity of acetyl CoA carboxylase (ACC) and/or amount of phosphorylated ACC enzyme in the animal, tissue or cell. The method is useful for identifying a compound that enhances or reduces whole body insulin sensitivity of an animal, and for preparing a composition for the treatment of obesity, diabetes, atherosclerosis and heart disease. The present amino acid sequence represents a human ACC2
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Ä 2483 Sequence

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                                                                      LAASKHKIIFIGPPG-SAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD
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                                                                                                                                                         LGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHOKIIEEA
                                                                                                                                                                 17;
 Length
                 Indels
                                                                                                                                                                                                                               Score 1669.5; DB 9
Pred. No. 1.8e-146;
; Mismatches 117;
               79;
57.4%;
       1 Similarity 60.8
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The invention relates to a novel peptide (I) comprising an acetyl CoA carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxylase (ACCase) having a deleted biotin binding domain, having a deleted carboxylase domain, and having a functional biotin carboxylase domain. A peptide of the invention is useful for identifying Acetyl CoA carboxylase inhibitors or activators, which involves combining the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, the presence of binding indicating the compound is or may be an Acetyl CoA carboxylase inhibitor or activator. The method further involves employing the identified binding compound in an assay to detect inhibition or enhancement of Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase activity, and selecting a compound that inhibits or activates Acetyl CoA carboxylase compound to be tested for the ability to bind to the biotin carboxylase domain, under conditions that permit binding to the biotin carboxylase domain, determining whether or not the compound binds to the biotin carboxylase domain, determining whether or not the compound in an assay to detect inhibition of Acetyl CoA carboxylase activity, and selecting a compound the inhibits Acetyl CoA carboxylase activity, and selecting a compound that inhibits Acetyl CoA carboxylase activity. The present sequence that inhibits and Accase BC domain of the invention.

Novel peptide comprising acetyl CoA carboxylase (ACCase) having delabiotin binding domain and carboxy transferase domain, and having functional biotin carboxylase domain, useful for identifying ACCase

9; SEQ ID NO 4; 56pp; English

Claim

inhibitors/activators.

SC;

Weatherly

SL,

Volrath

Elich TD,

WPI; 2004-180421/17

2002US-0401170P

(CROP-) CROPSOLUTION

2003WO-US024356

04-AUG-2003;

12-FEB-2004

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                                                                               15 NPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAIEFT
                                                                                                                        NPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETMMSD
                                                    QGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQLYN
                                                                                                                                                                          200 DG---IPDEIYNAAMLRDGQHCLDECKRIGFPVMIKASEGGGGKGIRMVHEESQVLSAWE
                                                                                                                                                                                                                 AVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQKIIEEAPVTI
                     18;
Length 555;
                    Indels
ch 55.2%; Score 1604; DB 8; l Similarity 58.2%; Pred. No. 2.2e-141; 309; Conservative 81; Mismatches 123;
                   81;
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carboxy transferase main; fungicide.

carboxylase; carbox domain; BC domain;

; Acetyl CoA carboxylase

ACCase; biotin

Phytophthora infestans

WO2004013159-A2

NO:4

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BC domain SEQ

ACCase

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Sequence 555

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any of the nucleotide sequences given in the specification in the individual nucleotide sequences given in the specification in the individual. The inventance of the SNP is correlated with an altered risk for myocardial infarction in the individual. The inventance of the specification or its complement and encoding any one of the amia acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an another specification and which is between about 16 and 1000 nucleotides in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SN nucleic acid molecule; a method of detecting a variant polypeptide; method for identifying an agent useful in treating or preventing method for identifying an agent useful in treating or preventing action method has cardiant action method for identifying an agent useful in treating or preventing and action method has cardiant action method for identifying an agent useful in treating or preventing and action method has cardiant action method for identifying and identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identify method identified in method identify method identified method identified in method identified method identified
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method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: sequence was not shown in the specification. The sequence has come from electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                             LKVNADYIRMADQYVEVPGGSNNNNYANVDLIVDVAERAGVHAVWAGWGHASENPRLPES
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                                                                                                                                                                                                          The invention relates to novel human secreted polypeptides. The polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins of the proteins and therapy, and can be used to express them are also useful for producing the proteins are used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias.

AAU29510-AAU33304 represent the amino acid sequences of novel human corrected proteins of the invention
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                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSDQGFLTVSDDVYQQACIHTAEEGLEKAEKIGYPVMIKASEGGGGKGIRKCTNGEEFKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASENPRLPESLAASKHKIIFIGPPGSAMRSLGDKISSTIVAQHADVPCMPWSGTGIKETM
                                                                                                                                                                                                                                                                                                      metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGGNPLETAPASPVADFIRKQGGHSVITKVLICNNGIAAVKEIRSIRKWAYETFGDERAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acetyl CoA carboxylase (ACC) is an enzyme which appears to be part of lipid storage system. ACC is end product regulated and is also the limiting enzyme in de novo fatty acid biosynthesis. A changed enzyme interfere with both the lipid and fatty acid metabolism in plants. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - is useful conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2240;
                                                                                                                                                                                                                                                                                                    acid; biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acetyl CoA-carboxylase from plants, e.g. brassica napus modifying the oil and fatty acid prodn. in plants or for resistance to certain herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.5%; Score 1583; DB 2;
larity 53.5%; Pred. No. 2.2e-138;
Conservative 105; Mismatches 146;
                                                                                                                                                                                                                                                                                                    carboxylase; lipid; fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ن</u>
                                                                                                                                                                2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; 31pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93DE-04301694
                                                                                                                                                                                                                                                                                                                                                                                                                                         93DE-04317260
                                                                                                                                                                 standard; protein;
                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                      carboxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schulte W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-236136/29
N-PSDB; AAQ67676.
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293; Conserv
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                                                                                      750
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                                                                                                                                                                                                                                                                                                                                                Brassica napus
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                                                                                                                                                                                                                                                                                                  COA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-1993;
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01-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-1994
                                                                                                                                                                                                                                                                      COA
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modifying
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Best Local S
Matches 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
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lant
                                 ADRSEARKOMVISLKELSIRGDFRTTVEYLIKLLETDAFESNKITTGWLDGLIQDRLTAE
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                                                                                                                     VSGVNIPAAOLOVAMGIPLYSIRDIRTLYGMDPRGNEVIDFDFSSPESFKTQRKPQPQGH
                                                                                                                                                                     VVACRITAENPDIGFKPGMGALTELNFRSSTSTWGYFSVGTSGALHEYADSQFGHIFAYG
                                                                                                                                                                                 CVAVRVTSEDPDDGFKPTSGQVQELSFKSNPNVWGYFSVKSGGGIHEFSDSQFGHVFAFG
                       IIEEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequent from plant with nucleic acid or amino acid sequencor plant organisms.
                      LYNAVLGEVPGSPVFVMKLAGQARHLEVQLLADQYGNAISIFGRDCSVQRRHQK
PPGSSLVTIPEEMYRQACVYTTEEAVASCQVVGYPAMIKASWGGGGKGIRKVHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; SEQ ID NO 462; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Herbicidally active polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                         2359 AA
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                                                                                                                                                                                                                                                                                                                                                         standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis
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                                                  110 VNGYHSDVVÞGRNVAEVNEFCKALGGKRPIHSILVATNGMAAVKFÍRSVRTWAYETFGSE
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 2359
 Length
                  Indels
DB 5;
-138;
137;
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Score 1581.5; D
Pred. No. 3.3e-1
5; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                   4, 2006, 18:08:37
               95;
Query Match
Best Local Similarity 53.3%;
Matches 305; Conservative
                                  IGGNPLETAPASPVA-
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ne : 208 secs
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